

REPLACEMENT SHEET

Figure 2. Sequence of C5 H6p WNV *prM-M-E* C5 in pDS-2646-1-1

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=>C5R
1  TGAATGTTAA ATGTTTACT TTGGATGAAG CTATAAATAT GCATTGGAAA AATAATCCAT
61  TTAAGGAAAG GATTCAAATA CTACAAAACC TAAGCGATAA TATGTTAACT AAGCTTATTC
121 TTAACGACGC TTAAATATA CACAAATAAA CATAATTTTT GTATAACCTA ACAAATAACT
181 AAAACATAAB AATAATAAAA GGAATGTAA TATCGTAATT ATTTTACTCA GGAATGGGGT
241 TAAATATTTA TATCACGTGT ATATCTATAC TGTTCGTGA TACTCTTTAC AATTACTATT
301 ACGAATATGC AAGAGATAAT AAGATTACGT ATTTAAGAGA ATCTTGTCAT GATAATTGGG
361 TACGACATAG TGATAAATGC TATTTCCGAT CGTTACATAA AGTCAGTTGG AAAGATGGAT
421 TTGACAGATG TAACCTAATA GGTGCAAAAA TGTTAAATAA CAGCATTCTA TCGGAAGATA
481 GGTACCACT TATATTATAC AAAATCACT GGTTCGATAA AACAGATTCT GCAATATTCG
541 TAAAGATGA AGATTACTGC GAATTTGTAA ACTATGACAA TAAAGGCCA TTTATCTCAA
601 CGACATCGTG TAATTTCTCC ATGTTTTATG TATGTGTTTC AGATATTATG AGATTACTAT
661 AAACCTTTTG TATACTTATA TTCCGTAAAC TATATTAATC ATGAAGAAAA TGAAAAAGTA
721 TAGAASCCTG TCACGAGCGG TTGTTGAAAA CAACAAAATT ATACATTCAA GATGGCTTAC
781 ATATAGCTCT GTGAGGCTAT CATGGATAAT GACAATGCAT CTCTAAATAG GTTTTGGAC
841 AATGGATTGC ACCCTAACAC GGAATATGCT ACTCTACAAT CTCTCTTTGA AATGGCTSTA
901 ATGTTCAAGA ATACCGAGGC TATAAAAATC TTGATGAGGT ATGGAGCTAA ACCTGTAGTT
961 ACTGAATGCA CAACCTCTTG TCTGCATGAT GCGGTGTTGA GAGACGACTA CAAAATAGTG
1021 AAAGATCTGT TGAAGAATAA CTATGTAAAC AATGTTCTTT ACAGCGAGG CTTTACTCCT
1081 TTGTGTTTGG CAGCTTACCT TAACAAAGTT AATTTGGTTA AACTTCTATT GGCTCATTGC
1141 GCGGATGTAG ATATTTCAAA CACGGATCGG TTAACCTCCT TACATATAGC CGTATCAAAT
1201 AAAAATTTAA CAATGGTTAA ACTTCTATT AACAAAGTG CTGATACTGA CTGTCTGGAT
1261 AACATGGGAC GTACTCTTTT AATGATCGCT GTACAATCTG GAATATTTGA AATATGTAGC
1321 ACACTACTTA AAAAAAATAA AATGTCCAGA ACTGGGAAAA ATTGATCTTG CCAGCTGTAA
1381 TTCTGTGTAG AAAAGAAAGT CTCAGGCTAC TTTTCAACAA AAGAGCAGAT GTAAACTACA
1441 TCTTTGAAAG AAATGGAAAA TCATATACTG TTTTGAATTT GATTAAAGAA AGTTACTCTG
1501 AGACACAAAA GAGGTAGCTG AATGGTACT CTCAAAAAGG TACGTGACTA ATTAGCTATA
1561 AAAAGGATCC GGGTTAATTA ATTAGTCATC AGGCAGGCGC AGAACGAGAC TATCTGCTCG

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Figure 2 continued

1621 TTAATTAATT AGAGCTTCTT ^{⇒H6p} TATTCTATAC TTAAAAGTG AAAATAAATA CAAAGGTTCCT
 1681 TGAGGGTGTG GTTAAATFGA AAGCGAGAAA TAATCATATA TTATTTTCATT ATCGCGAATAT
 1741 CCGTTAAGTT TGTATCGTAA ^{⇒ WNIV capsid leader} TGACCGGAAT TGCAGTCATG ATTGGCCTGA TCGCCAGCGT
 1801 . G A V T L S N F Q G K V M M T V N A T D .
 AGGAGCAGTT ACCCTCTCTA ACTTCCAAGG GAAGGTGATG ATGACGGTAA ATGCTACTGA
 1861 . V T D V I T I P T A A G K N L C I V R A .
 CGTCACAGAT GTCAACAGA TTCCAACAGC TGCTGGAAAG AACCTATGCA TTGTGACAGC
 1921 . M D V G Y M C D D T I T Y E C P V L S A .
 AATGGATGTG GGATACATGT GCGATGATC TATCACTTAT GAATGCCAGC TGCTGTCGGC
 1981 . G N D P E D I D C W C T K S A V Y V R Y .
 TGGAATGAT CCAGAAGACA TCGACTGTTG GTGCACAAAG TCAGCAGTCT ACGTCAGGTA
 2041 . G R C T K T R H S R R S R R ^{⇒ WNIV M} S L T V Q T .
 TGGAAGATGC ACCAAGACAC GCCACTCAAG ACGCAGTCGG AGGTCACTGA CTGTGACAGC
 2101 . H G E S T L A N K K G A W M D S T K A T .
 ACACGGAGAA AGCACTCTAG CGAACAGAA GGGGGCTTGG ATGACAGCA CCAAGGCCAC
 2161 . R Y L V K T E S W I L R N P G Y A L V A .
 AAGGTATTTG GTAAAAACAG AATCATGGAT CTTGAGGAAC CCTGGATATG CCTGGTGGC
 2221 . A V I G W M L G S N T M Q R V V F V V L .
 AGCGGTCTAT GGTGATGTC TTGGAGCAA CACCATGCAG AGAGTTGTGT TTGCTGTGCT
 2281 . L L L V A P A Y S F N C L G M S N R D F .
 ATTGCTTTTG GTGGCCCGAG CTTACAGCTT CAACTGCCTT GGAATGAGCA ACAGAGACTT
 2341 . L E G V S G A T W V D L V L E G D S C V .
 CTTGGAAGGA GTGTCGGAG CACATGGGT GGATTGCGTT CTCGAGGCG ACAGCTGCGT
 2401 . T I M S K D K P T I D V K M M N M E A A .
 GACTATCATG TCTAAGGACA AGCTTACCAT CGATGTGAAG ATGATGAATA TGGAGGCGGC
 2461 . N L A E V R S Y C Y L A T V S D L S T K .
 CAACCTGGCA GAGGTCGCA GTTATTGCTA TTTGGCTACC GTCAGCGATC TCTCCACCAA
 2521 . A A C P T M G E A H N D K R A D P A F V .
 AGCTGCGTGC CCGACCATGG GAGAAGCTCA CAATGACAAA CGTGTGACC CAGCTTTTGT
 2581 . C R Q G V V D R G W G N G C G L F G K G .
 GTGCAGACAA GGAGTGGTG ACAGGGGCTG GGGCAACGGC TGCAGGACTAT TTGGCAAAGG

REPLACEMENT SHEET

Figure 2 continued

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. S I D T C A K F A C S T K A I G R T I L .
2641 AAGCATTGAC ACATGCGCCA AATTGCGCTG CTCTACCAAG GCAATAGGAA GAACCATCTT
      mutated T5NT
. K E N I K Y E V A I F V H G P T T V E S .
2701 GAAAGAGAAT ATCAAGTACG AAGTGGCCAT CTCTGTCGAC GGACCAACTA CTGTGGAGTC

. H G N Y S T Q V G A T Q A G R F S I T P .
2761 GCACGGAAC TACTCCACAC AGGTGGAGC CACTCAGGCA GGGAGATTCA GCATCACTCC

. A A P S Y T L K L G E Y G E V T V D C E .
2821 TGGGCGCCT TCATACACAC TAAAGCTTGG AGAATATGGA GAGGTGACAG TGGACTGTGA

. P R S G I D T N A Y Y V M T V G T K T F .
2881 ACCACGGTCA GGGATTGACA CCAATGCATA CTACGTGATG ACTGTGGAA CAAAGACGTT

. L V H R E W F M D L N L P W S S A G S T .
2941 CTTGGTCCAT CGTGAGTGGT TCATGGACCT CAACCTCCCT TGGAGCAGTG CTGGAAGTAC

. V W R N R E T L M E F E E P H A T K Q S .
3001 TGTGTGGAGG AACAGAGAGA CGTTAATGGA GTTTGAGGAA CCACACGCCA CGAAGCAGTC

. V I A L G S Q E G A L H Q A L A G A I P .
3061 TGTGATAGCA TTGGGCTCAC AAGAGGGAGC TCTGCATCAA GCTTTGGGTG GAGCCATTCC

. V E F S S N T V K L T S G H L K C R V K .
3121 TGTGGAATTT TCAAGCAACA CTGTCAAGTT GACGTCGGGT CATTTGAAGT GTAGAGTGAA

. M E K L Q L K G T T Y G V C S K A F K F .
3181 GATGGAAAAA TTGCAGTTGA AGGGAACAAC CTATGGCGTC TGTTCAAAGG CTTTCAAGTT

. L G T P A D T G H G T V V L E L Q Y T G .
3241 TCTTGGGACT CCCGACAGACA CAGGTCACGG CACTGTGGTG TTGGAATTGC AGTACACTGG

. T D G P C K V P I S S A A S L N D L T P .
3301 CACGGATGGA CCTTGAACAAG TTCCATCTC GTACGCGGCT TCATTGAACG ACCTAACGCC

. V G R L V T V N P F V S V A T A N A K V .
3361 AGTGGGCAGA TTGGTCACTG TCAACCCTTT TGTTCAGTG GCCACGGCCA ACGCTAAGGT

. L I E L E P P F G D S Y I V V G R G E Q .
3421 CCTGATTGAA TTGGAACCAC CCTTTGAGA CTCATACATA GTGTGGGCA GAGGAGAACA

. Q I N H H W H K S G S S I G K A F T T T .
3481 ACAGATCAAT CACCATTGGC ACAAGTCTGG AGCAGCATT GGCAAAAGCCT TTACAACCAC

. L K G A Q R L A A L G D T A W D F G S V .
3541 CCTCAAAGGA GCGCAGAGAC TAGCCGCTCT AGGAGACACA GCTTGGGACT TTGGATCAGT

. G G V F T S V G K A V H Q V F G G A F R .
3601 TGGAGGGGTG TTCACTCAG TTGGAAGGC TGTCCATCAA GTGTTCGGAG GAGCATCCG

. S L F G G M S W I T Q G L L G A L L L W .
3661 CTCACGTGTC GGAGGCATGT CTTGGATAAC GCAAGGATTG CTGGGGGCTC TCCTGTGTG

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REPLACEMENT SHEET

Figure 2 continued

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      . M G I N A R D R S I A L T F L A V G G V .
3721  GATGGGCATC AATGCTCGTG ATAGGTCCAT AGCTCTCACG TTTCTCGCAG TTGGAGGAGT

      . L L F L S V N V H A
3781  TCTGCTCTTC CTCTCCGTGA ACGTGCACGC TTAATTTTAA TCTAGAATCG ATCCCGGGTT
      => G5L
3841  TTTATGACTA GTTAATCACG GCCGCCTTAT AAAGATCTAA AATGCATAAT TTCTAALTA
3901  TGAATAAAAG TACATCATGA GCAACGCGTT AGTATATTTT ACAATGGAGA TTACCGCTCT
3961  ATACCGTTCT ATGTTTATTG ATTCAGATGA TGTTTAGAA AAGAAAGTTA TTGAATATGA
4021  AAACCTTAAT GAAGATGAAG ATGAGGACGA TGATTATTGT TGTAAATCTG TTTTAGATGA
4081  AGAAGATGAC GCGCTAAAGT ATACTATGGT TACAAAGTAT AAGTCTATAC TACTAATGGC
4141  GACTTGTGCA AGAAGGTATA GTATAGTGAA AATGTTGTTA GATTATGATT ATGAAAAACC
4201  AARTAAATCA GATCCATATC TAAAGGTATC TCCTTTGCAC ATAATTTCAT CTATTCTAG
4261  TTTAGAATAC

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REPLACEMENT SHEET

Figure 4. Sequence of F8 H6p WNV prM-M-E F8 in pSL-5513-1-1-1.

⇒ F8E

1 GACCCCTTTC AAGAATRAAA GAAGAAACAA CTGTGAAATA GTTTATAAAT GTAAITCGTA

61 TGCAGAAAAC GATAATATAT TTTGGTATGA GAAATCTRAA GGAGACATAG TTTGTATAGA

121 CATGCGCTCT TCCGATGAGA TATTGATGC TTTTCTAATG TATCATATAG CTACAAGATA

181 TGCCTATCAT GATGATGATA TATATCTACA AATAGTGTTA TATTATTCTA ATAATCAAAA

241 TGGTATATCT TATATTACGA AAAATAAATA CGTTAAGTAT ATAAGARAATA AAACATAGAGA

301 CGATATTTCAT AAAGTAAAAA TATTAGCTCT AGAAGACTTT ACAACGGAAG AAATATATTG

361 TTGCATTAGT AATATATAAC AGCGTAGCTG CACGGTTTTC ATCATTTTCC AACAAATATA

421 ACCAATGAAG GAGGACGACT CATCAACAT AAATAACATT CACGGAAAAA ATTCAGTATC

481 AGATTTTATCA CAAGATGATT ATGTTATTGA ATGTATAGAC GGATCTTTTG ATTCGATCAA

541 GTATAGAGAT ATAAAGGTTA TAATATGAA GAATAACGGT TACGTTAATT GTAGTAAATT

601 ATGTAAATG CGGAATAAAT ACTTTTCTAG ATGGTTGCGT CTTTCTACTT CTAAAGCATT

661 ATTAGACATT TACAATAATA AGTCAGTAGA TAATGCTATT GTTAAAGTCT ATGTTAAAGG

721 TAAGAAACTT ATTATAACAG GATTTTATCT CAAACAAAAT ATGATACGTT ATGTTATTGA

781 GTGGATAGGG GATGATTTTA CAAACGATAT ATACAAAATG ATTAATTTCT ATAATGGTT

841 ATTCGGTAAC GATGAATTAA AAATAGTATC CTGTGAAAC ACTCTATGCC CGTTTATAGA

901 ACTTGTAGTA TGCTATTATG GTAAAAAATG TAAGTATATA CACGGAGATC AATGTGATAT

961 CTGTGGTCTA TATATACTAC ACCCTACCGA TATTAACCAA CGAGTTTCTC ACAAGAAAAA

1021 TTGTTTAGTA GATAGAGATT CTTTGATTGT GTTTAAAAGA AGTACCAGTA AAAAGTGTGG

1081 CATATGCATA GAAGAAATAA ACAAAAACA TATTTCCGAA CAGTATTTTG GAATCTCTCC

1141 AAGTTGTAAA CATATTTTTT GCCTATCATG TATAAGACGT TGGGACAGATA CTACCAGAAA

1201 TACAGATACT GAAAATACGT GTCCGTAATG TAGAATAGTT TTTCCCTTCA TAATACCCAG

1261 TAGGTATTGG ATAGATAATA AATATGATRA AAAAAATTA TATAATAGAT ATAAGAAAAA

1321 GATTTTTCATA AAAATACCTA TAAGAACAAT AAAAAATATA TTACATTTAC GGAAAAATAG

1381 TGGTTTTAGT TTACCAACTT AGAGTAATTA TCATATTGAA TCTATATTGC TAATTAGCTA

1441 ATAAAAACCC GGGTTAATTA ATTAGTCATC AGGCAGGGCG AGAACGAGAC TATCTGCTCG

⇒ H6E

1501 TTAATTAATT AGAGCTCTTT TATTCCTATC TTAAAAAGTG AAAATAATA CAAGGTTCT

REPLACEMENT SHEET

Figure 4 continued

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1561  TGAGGGTGTG GTTAAATTGA AAGCGAGAAA TAATCATATAA TTATTTCATT ATCGCGATAT
                                     => WNV capsid leader
                                     M T G I A V M I G L I A S V .
1621  CCGTTAAGTT TGTATCGTAA TGACCGGAAT TGCAGTCATG ATTGGCCTGA TCGCCAGCGT
                                     => WNV p1M
. G A V T L S N F Q G K V M M T V N A T D .
1681  AGGAGCGGTT ACCTCTCTA ACTTCCAAGG GAAGGTGATG ATGACGGTAA ATGCTACTGA
. V T D V I T I P T A A G K N L C I V R A .
1741  CGTCACAGAT GTCATCACGA TTCCAACAGC TGCTGAAAG AACCTATGCA TTGTGAGAGC
. M D V G Y M C D D T I T Y E C P V L S A .
1801  AATGGATGTG GGATACATGT GCGATGATAC TATCACTTAT GAATGCCAG TGCTGTGGGC
. G N D P E D I D C W C T K S A V Y V R Y .
1861  TGGTAATGAT CCAGAAGACA TCGACTGTGT GTGCACAAAG TCAGCAGTCT ACGTCAGGTA
                                     => WNV M
. G R C T K T R H S R R S R R S L T V Q T .
1921  TGAAGATGC ACCAAGACAC GCCACTCAAG ACGCAGTCGG AGCTACTGCA CAGTCAGAGC
. H G E S T L A N K K G A W M D S T K A T .
1981  ACACGGAGAA AGCACTCTAG CGAACAAGAA GGGGGCTTGG ATGGACAGCA CCAAGGCCAC
. R Y L V K T E S W I L R N P G Y A L V A .
2041  AAGGTATTTG GTAAAAACAG AATCATGGAT CTTGAGGAAC CTGGATATG CCCTGCTGGC
. A V I G W M L G S N T M Q R V V F V V L .
2101  AGCCGTCATT GGTGGATGC TTGGGAGCAA CACCATGCAG AGAGTTGTGT TTGCTGCTGT
                                     => WNV E
. L L L V A P A Y S F N C L G M S N R D F .
2161  ATTGCTTTTG GTGGCCCCAG CTTACAGCTT CAACTGCCTT GGAATGAGCA ACAGAGACTT
. L E G V S G A T W V D L V L E G D S C V .
2221  CTGGGAAGGA GTGTCGGAG CAACATGGGT GGATTTGGTT CFCAGAGCG ACAGCTGCGT
. T I M S K D K P T I D V K M M N M E A A .
2281  GACTATCATG TCTAAGGACA AGCCTACCAT CGATGTGAAG ATGATGAATA TGGAGGGGGC
. N L A E V R S Y C Y L A T V S D L S T K .
2341  CAACCTGGCA GAGGTCCGCA GTTATTGCTA TTTGGCTACC GTCAGGATC TCTCCACCAA
. A A C P T M G E A H N D K R A D P A F V .
2401  AGCTGCGTGC CCGACCATGG GAGAAGCTCA CAATGACAAA CGTGTGACC CAGCTTTTGT
. C R Q G V V D R G W G N G C G L F G K G .
2461  GTGCAGACAA GGAGTGGTGG ACAGGGGCTG GGGCAACGGC TCGGAGTAT TTGGCAAAGG
. S I D T C A K F A C S T K A I G R T I L .
2521  AAGCATTGAC ACATGGGCCA AATTTGCCGT CTCTACCAAG GCAATAGGAA GAACCATCTT

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REPLACEMENT SHEET

Figure 4 continued

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. K E N I K Y E V A I F V H G P T T V E S .
2581 GAAAGAGAAT ATCAAGTACG AAGTGGCCAT CTTCGTGCAC GGACCAACTA CTGTGGAGTC

. H G N Y S T Q V G A T Q A G R F S I T P .
2641 GCACGGAAAC TACTCCACAC AGGTGGAGC CACTCAGGCA GGGAGATTCA GCATCACTCC

. A A P S Y T L K L G E Y G E V T V D C E .
2701 TGGCGGCCCT TCATACACAC TAAAGCTTGG AGAATATGGA GAGGTGACAG TGGACTGTGA

. P R S G I D T N A Y Y V M T V G T K T F .
2761 ACCACGGTCA GGGATTGACA CCAATGCATA CTACGTGATG ACTGTTGGAA CAAAGACGTT

. L V H R E W F M D L N L P W S S A G S T .
2821 CTGTGTCCAT CGTGAGTGGT TCATGGACCT CAACCTCCCT TGGAGCAGTG CTGGAAGTAC

. V W R N R E T L M E F E E P H A T K Q S .
2881 TGTGTGGAGG AACAGAGAGA CGTTAATGGA GTTTGAGGAA CCACACGCCA CGAAGCAGTC

. V I A L G S Q E G A L H Q A L A G A I P .
2941 TGTGATGACA TTGGGCTCAC AAGAGGGAGC TCTGCATCAA GCTTTGGCTG GAGCCATTCC

. V E F S S N T V K L T S G H L K C R V K .
3001 TGTGGAAATT TCAAGCAACA CTGTCAAGTT GACGTCGGGT CATTTGAAGT GTAGAGTGAA

. M E K L Q L K G T T Y G V C S K A F K F .
3061 GATGGAAAAA TTGCAGTTGA AGGGAACAAC CTATGGCGTC TGTTCAAAGG CTTTCAAGTT

. L G T P A D T G H G T V V L E L Q Y T G .
3121 TCITGGGACT CCCGAGACA CAGGTCACGG CACTGTGGTG TTGGAATTGC AGTACACTGG

. T D G P C K V P I S S A A S L N D L T P .
3181 CACGGATGGA CCTTGCAAAG TTCCTATCTC GTCAGCGGCT TCATTGAACG ACCTAACGCC

. V G R L V T V N P F V S V A T A N A K V .
3241 AGTGGCAGA TTGGTCACTG TCAACCCITT TGTTCAGTG GCCACGGCCA ACGCTAAGGT

. L I E L E P P F G D S Y I V V G R G E Q .
3301 CCTGATTGAA TTGGAACCAC CCTTTGGAGA CTCATACATA GTGGTGGGCA GAGGAGAACA

. Q I N H H W H K S G S S I G K A F T T T .
3361 ACAGATCAAT CACCATTTGC ACAAGTCTGG AAGCAGCATT GGCAAAGCCT TTACAACCAC

. L K G A Q R L A A L G D T A W D F G S V .
3421 CCTCAAAGGA GCGCAGAGAC TAGCCGCTCT AGSAGACACA GCTTGGGACT TTGGATCAGT

. G G V F T S V G K A V H Q V F G G A F R .
3481 TGGAGGGGTG TTCACCTCAG TTGGGAAGGC TGTCCATCAA GTGTTCCGAG GAGCATTCCG

. S L F G G M S W I T Q G L L G A L L L W .
3541 CTCACPTGTC GGAGGCATGT CCTGGATAAC GCAAGGATTG CTGGGGGCTC TCCTGTPTGT

. M G I N A R D R S I A L T F L A V G G V .
3601 GATGGGCATC AATGCTCGTG ATAGTCCAT AGCTCTCACG TTTCTCGCAG TTGGAGGAGT

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REPLACEMENT SHEET

Figure 4 continued

	. L L F L S V N V H A
3661	TCTGCTCTTC CTCTCCGTGA ACGTGCACGC TTAATTTTTA TCTAGAGTCG AGTTTTTATT
	⇒ FRL
3721	GACTAGTTAA TCATAAGATA AATAATATAC AGCATTGTAA CGATCGTCAAT CGGTATATACG
3781	GGGAATAATA TTACCATACA GTATTATTAA ATTTCTTTAC GAAGAATATA GATCGGTATT
3841	TATCGTTAGT TTATTTTACA TTTATTAATT AAACATGCTT ACTATTACCT GTATCGGAAA
3901	TCACAAATTT AGTTATATAA TTTATGATAA AATTAAGATA ATAATATGA AATCAATAAA
3961	TTATGTTAAT GCTACTAGAT TATGTGAATT ACGAGGAAGA AAGTTTACGA ACTGGAAAAA
4021	ATTAAGTGAA TCATAAATAT TAGTCGATAA TGTAAAAAAA ATAAATGATA AAACATAACA
4081	GTAAAAACG GATATGATTA TATACGTTAA GGATATTGAT CATAAGGAA GAGATCTTTG
4141	CGGTTACTAT GTACACCAAG ATCTGGTATC TTCTATATCA AATTGGATAT CTCCGTTATT
4201	CGCGGTTAAG GTAAATAAAA TTATTTAATA TTATATATGT AATGAATATG ATATACGACT
4261	TAGCGAAATG GAATCTGATA TGACAGAACT AATAGATGTA GTTGATAAAT TAGTAGGAGG
4321	ATACAAATGAT GAATATGACG AATAAATATA TTTCTTTAAT AAATTTATAG AAAAATATAT
4381	TGCTAACATA TCGTTATCAA CTGAATTATC TAGTATATTA AATAATTTTA TAAATTTTAA
4441	TAAAAAATAC AATAACGACA TAAAGATAT TAAATCTTTA ATTCTTGATC TGAAAAACAC
4501	ATCTATATTA CTAGATAAAA AGTTATTCTG TAAAGATAAT AATGAATCGA ACGATGAAAA
4561	ATTGGAACCA GAAGTTGATA AGCTAATTTT TTCTATCTAA ATAGTATTAT TTTATTGAAG
4621	TACGAAGTTT TACGTTAGAT AAATAATAAA GGTCGATTTT TACTTTGTTA AATATCAAA
4681	ATCTCATTAT CTGATAAAGA TACAAAAACA CACGGTGATT ATCAACCATC TAACGAACAG
4741	ATATTACAAA AAATACGTCG GACTATGGAA AACGAAGCTG ATAGCCTCAA TAGAAGAAGC
4801	ATTAAAGAAA TTGTTGTAGA TGTATGAGG AATTGGGATC ATCTCTCTAA CGAAGAAATA
4861	GATAAAGTTT TAAACTGGAA AATGATACA TTAACGATTT TAGATCATCT AAATACAGAT
4921	GATAATATTA AGGAAATCAT ACAATGCTCG ATTAGAGAAAT TTGCGTTTAA AAAGATCAAT
4981	TCTATTATGT ATAGTTATGC TATGGTAAAA CTCATTCAG ATAACGAAC ATTGAAAGAT
5041	AAAATTAAGG ATTTATTTTAT AGAAATATTT CTTAAAGACA AACCTGGTTA TAAACAAAA
5101	CGATTACCC

REPLACEMENT SHEET

Figure 8. Nucleotide sequence and translation of the WNV *prM-M-E* region in pSL-5448-1-1, pVR1012 WNV *prM-M-E*.

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PstI      Kozak      ⇒ WNV capsid leader
1  CTGCAGCCGC CACCATGGGA TCAACCGGAA TTGCAGTCAT GATTGGCCCTG ATCGCTCAGG

⇒ WNV prM
61  .. G A V T L S N F Q G K V M M T V N A T D .
    TAGGAGCAGT TACCCTCTCT AACTTCCAAG GGAAGGTGAT GATGACGGTA AATGCTACTG

121  .. V T D V I T I P T A A G K N L C I V R A .
    ACGTCACAGA TGTCAATCAG ATTCCAACAG CTGCTGGAAA GACCATATGC ATTGTCAGAG

    .. M D V G Y M C D D T I T Y E C P V L S A .
181  CAATGGATGT GGGATACATG TCGATGATA CTATCACTTA TGAATGCCA GTGCTGTCGG

    .. G N D P E D I D C W C T K S A V Y V R Y .
241  CTGGTAATGA TCCAGAAGAC ATCGACTGTT GGTGCACAAA GTCAGCAGTC TACGTCAGGT

⇒ WNV M
301  .. G R C T K T R H S R R S R R S L T V Q T .
    ATGGAAGATG CACCAAGACA CGCCACTCAA GACGAGTCG GAGGTCAGTG ACAGTGCAGA

361  .. H G E S T L A N K K G A W M D S T K A T .
    CACACGGAGA AAGCACTCTA GCGAACAAGA AGGGGGCTTG GATGGACAGC ACCAAGGCCA

    .. R Y L V K T E S W I L R N P G Y A L V A .
421  CAAGGTATTT GGTAAAAACA GAATCATGGA TCTTGAGGAA CCCTGGATAT GCCCTGCTGG

    .. A V I G W M L G S N T M Q R V V F V V L .
481  CAGCCGTCAT TGGTTGGATG CTTGGGAGCA ACACCATGCA GAGAGTTGTG TTTGCTGTGC

⇒ WNV E
541  .. L L L V A P A Y S F N C L G M S N R D F .
    TATTGCTTTT GGTGGCCCCA GCTTACAGCT TCACTGCTCT TGGAATGAGC AACAGAGACT

601  .. L E G V S G A T W V D L V L E G D S C V .
    TCTTGGAAAG AGTGTCTGGA GCRACATGGG TGGATTGGT TCTCGAAGGC GACAGCTGCG

ClnI
661  .. T I M S K D K P T I D V K M M N M E A A .
    TGACTATCAT GTCTAAGGAC AAGCCTACCA TCGATGTGAA GATGATGAAT ATGGAGCGCG

    .. N L A E V R S Y C Y L A T V S D L S T K .
721  CCAACCTGGC AGAGGTCGCG AGTATTGCT ATTTGGCTAC CGTCAGCGAT CTCCTCCACCA

    .. A A C P T M G E A H N D K R A D P A F V .
781  AAGTCTGCTG CCCGACCATG GGAGAAGCTC ACAATGACAA ACGTCTGTAC CCAGCTTTTG

841  .. C R Q G V V D R G W G H G C G L F G K G .
    TGTGCAGACA AGGAGTGTGT GACAGGGGCT GGGGCAACGG CTGCGGACTA TTTGGCAAG

    .. S I D T C A K F A C S T K A I G P T I L .
901  GAAGATTTGA CACATGCGCC AAATTTCGCT GCTCTACCAA GGCAATAGGA AGACCATCT

    .. K E N I K Y E V A I F V H G P T T V E S .
961  TGAAGAGAA TATCAAGTAC GAAGTGGCCA TTTTGTCCA TGACCAACT ACTGTGGAGT

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REPLACEMENT SHEET

Figure 8 continued

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1021 .. H G N Y S T Q V G A T Q A G R F S I T P .
CGCACGGAAA CTACTCCACA CAGGTGGAG CCACTCAGGC AGGGAGATTC AGCATCACTC

1081 .. A A P S Y T L K L G E Y G E V T V D C E .
CTGCGGCGCC TTCATACACA CTAAGCTTG GAGATATGG AGAGTGACA GTGGACTGTG

1141 .. P R S G I D T N A Y Y V M T V G T K T F .
AACCAGGTC AGGATTGAC ACCAATGCAT ACTACGTGT GACTGTGGA ACAAGACTG

1201 .. L V H R E W F M D L N L F W S S A G S T .
TCTTGGTCCA TCGTGAGTG TTCATGGACC TCAACCTCCC TIGGAGCAGT GCTGGAAGTA

1261 .. V W R N R E T L M E F E E F H A T K Q S .
CTGTGTGGAG GAACAGAGAG ACGTTAATGG AGTTTGAGGA ACCACACGCC ACGAAGCAGT

1321 .. V I A L G S Q E G A L H Q A L A G A I P .
CTGTGATAGC ATTGGGCTCA CAAGAGGGAG CTCTGCATCA AGCTTTGGCT GGAGCCATTC

1381 .. V E F S S N T V K L T S G R L K C R V K .
CTGTGGAATT TTCAGCAAC ACTGTCAAGT TGACGTCCGG TCATTGAAG TGTAGAGTGA

1441 .. M E K L Q L K G T T Y G V C S K A F K F .
AGAIGGAAAA ATTGCAGTTG AAGGGACAAA CCTATGGCGT CTGTTCAAGG GCTTTCAAGT

1501 .. L G T P A D T G H G T V V L E L Q Y T G .
TTCTTGGGAC TCCCGCAGAC ACAGGTCACG GCACTGTGGT GTTGAATTG CAGTACACTG

1561 .. T D G F P C K V P I S S A A S L N D L T P .
GCACGGATGG ACCTTGCAAA GTTCTATCT CGTCAGCGGC TTCATTGAAC GACCTAACGC

1621 .. V G R L V T V N P F V S V A T A N A K V .
CAGTGGGCGC ATTGGTCACT GTCAACCCCT TTGTTTCAGT GGCCACGECG AACGCTAAGG

1681 .. L I E L E P F F G D S Y I V V G R G E Q .
TCCTGATTGA ATTGGAACCA CCCTTTGGAG ACTCATACT AGTGTGGGG AGAGGAGAAC

1741 .. Q I U H R W H K S G S S I G K A F T T T .
AACAGATCAA TCACCATTGG CACAAGTCTG GAAGCAGCAT TGCCAAAGCC TTTACAACCA

1801 .. L K G A Q R L A A L G D T A W D F G S V .
CCCTCAAGAG AGCGCAGAGA CTAGCCGCTC TAGGAGACAC AGCTTGGGAC TTTGGATCAG

1861 .. G G V F T S V G K A V H Q V F G G A F R .
TTGGAGGGGT GTTCACCTCA GTTGGGAAGG CTGTCCATCA AGTGTTCGGA GGAGCATTC

1921 .. S L F G G M S W I T Q G L L G A L L L W .
GCTCACTGTT CGGAGGCATG TCCTGGATAA CGCAAGGATT GCTGGGGCT CTCTGTTGT

1981 .. M G I N A R D R S I A L T F L A V G G V .
GGATGGGCAT CAATGCTCGT GATAGGTCCA TAGCTCTCAC GTTTCTCGCA GTTGGAGGAG

2041 .. L L F L S V N V H A
TTCTGCTCTT CCTCTCCGTG AACGTGCACG CTTAATTTTT A[CTAGA]

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XbaI

REPLACEMENT SHEET

FIGURE 9
Sequence of pDS-2946-1-1, pC5 H6p WNV *prM-M-E*.

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1   GCGCCCAATACGCAAAACCGCCTCTCCCCGCGCGTTGGCCGATTCAATATGCAGCTGGCA
61  CGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCT
121 CACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAAT
                                     ⇨ C5R
181 TGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGAATTGCGGCC
241 GCAATTCTGAATGTTAAATGTTATACCTTGGATGAAGCTATAAATATGCATTGGAAAAAT
301 AATCCATTAAAGAAAGGATTCAATACTACAAAACCTAAGCGATAATATGTTAACTAAG
361 CTTATTCTTAAACGACGCTTAAATATACACAAATAAACATAAATTTTGTATAACCTAACA
421 AATAACTAAACATAAAAATAATAAAGGAAATGTAATATCGTAATTATTTTACTCAGGA
481 ATGGGGTTAAATATTTATATCACGTGTATATCTATACTGTTATCGTATACTCTTACAAT
541 TACTATTACGAATATGCAAGAGATAATAAGATTACGTATTTAAGAGAATCTTGTTCATGAT
601 AATTGGGTACGACATAGTGATAAATGCTATTTTCGCATCGTTACATAAAGTCAGTTGGAAA
661 GATGGATTGACAGATGTAACTTAATAGGTGCAAAAATGTTAAATAACAGCATTCTATCG
721 GAAGATAGGATACCACTTATATTATACAAAAATCACTGGTTGGATAAAAACAGATTCTGCA
781 ATATTCGTAAAAGATGAAGATTACTGCGAATTTGTAACTATGACAATAAAAAGCCATT
841 ATCTCAACGACATCGTGTAATCTTCCATGTTTATGTATGTGTTTCAGATATTATGAGA
901 TTACTATAAACTTTTTTGTACTTTATATTCGGTAACTATATTAATCATGAAGAAAATGA
961 AAAAGTATAGAAGCTGTTTCACGAGCGGTTGTTGAAAACAACAAATTTATACATTCAAGAT
1021 GGCTTACATATACGTCTGTGAGGCTATCATGGATAATGACAATGCATCTCTAAATAGGTT
1081 TTTGGCAATAGGATTGACCCCTAACACGGATATGGTACTCTCAATCTCCTCTTGAAT
1141 GGCTGTAAATGTTCAAGAATACCGAGGCTATAAAAATCTTGATGAGGTATGGAGCTAAACC
1201 TGTAGTTACTGAATGCACAACTTCTTGTCTGCATGATGCGGTGTTGAGAGACGACTACAA
1261 AATAGTGAAAGATCTGTTGAAGAATAACTATGTAACAATGTTCTTTACAGCGGAGGCTT
1321 TACTCCTTTGTGTTTGGCAGCTTACCTTAACAAAGTTAATTTGGTTAAACTTCTATTGGC
1381 TCATTGCGGCGGATGTAGATATTTCAACACGGATCGGTTAACTCCTCTACATATAGCCGT
1441 ATCAAATAAAAATTTAACAATGGTTAACTTCTATTGAACAAGGTGCTGATAGTACTT
1501 GCTGGATAACATGGGATGTACTCCTTTAATATACGCTGTACAACTCTGGAAATATTGAAAT

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REPLACEMENT SHEET

Figure 9 continued

1561 ATGTAGCACACTACTTAAATAAATAAATGTCCGAACTGGGAAAAATTGATCTTGCCA

1621 GCTGTAACTCATGGTAGAAAAGAGTCTCAGGCTACTTTTCAACAAAGGAGCAGATGTA

1681 AACTAATCTTTTGAAGAAATGGAAAAATCATATACTGTTTGGAAATTGATTAAAGAAAGT

1741 TACTCTGAGACACAAAAGAGGTAGCTGAATGGTACTCTCAAGGTACGTGACTAATTAG

1801 CTATATAAAGGATCCGGGTTAATTAATTAGTCATCAGGCAGGGCGAGAACGAGACTATCT

⇒ H6p

1861 GCTCGTTAATTAATTAGAGCTCTTTTCTTACTTAAAAAGTGAAAAATAATACAAG

1921 GTTCTTGAGGGTTGTGTTAAATTGAAAGCGAGAAATATCATAAATTATTTATTATTCGC

⇒ WNV capsid leader

M T G I A V M I G L I A

1981 GATATCCGTTAAGTTTGTATCGTAATAGCCGGAATTGCAGTCATGATTGGCTGATCGCC

⇒ WNV prM start

S V G A V T L S N F Q G K V M M T V N A

2041 AGCGTAGGAGCGTTACCTCTCTAACTTCCAAGGGAAGGTGATGATGACGGTAAATGCT

T D V T D V I T I P T A A G K N L C I V

2101 ACTGAGCTCAGATGTCATCAGATTCCAACAGCTGCTGGAAAGAACCTATGCAATTGTC

R A M D V G Y M C D D T I T Y E C P V L

2161 AGAGCAATGGATGTGGATACATGTGCGATGATACTATCAATTGAATGCCAGTGCTG

S A G N D P E D I D C W C T K S A V Y V

2221 TCGGCTGGTAATGATCCAGAAGACATCGACTGTTGGTGCACAAAGTCAGCAGTCTACGTC

⇒ WNV M start

R Y G R C T K T R H S R R S R R S L T V

2281 AGGTATGGAAGATGCACCAAGACACGCCACTCAAGACGAGTCGGAGGTCACAGAGTG

Q T H G E S T L A N K K G A W M D S T K

2341 CAGACACACGGAGAAAGCACTCTAGCGAACAAGAAGGGGGCTTGGATGGACAGCACCAAG

A T R Y L V K T E S W I L R N P G Y A L

2401 GCCACAAGGTATTGGTAAAAACAGAAATCATGGATCTTGAGGAACCTGGATATGCCCTG

V A A V I G W M L G S N T M Q R V V F V

2461 GTGGCAGCGTCATTGGTTGGATGCTTGGGAGCAACACCATGCAGAGAGTTGTGTTGTGTC

⇒ WNV E start

V L L L L V A P A Y S F N C L G M S N R

2521 GTGCTATTGCTTTTGGTGGCCCCAGCTTACAGCTTCAACTGCCTTGGAAATGAGCAACAGA

D F L E G V S G A T W V D L V L E G D S

2581 GACTTCTTGAAGGAGTGTCTGGAGCAACATGGGTGGATTTGGTTCTCGAAGGCGACAGC

REPLACEMENT SHEET

Figure 9 continued

C V T I M S K D K P T I D V K M M N M E
 2641 TGGCTGACTATCATGTCTAAGGACAAGCCTACCATCGATGTGAAGATGATGAATATGGAG

A A N L A E V R S Y C Y L A T V S D L S
 2701 GCGGCCAACCTGGCAGAGGTCCGCAGTTATTGCTATTTGGCTACCGTCAGCGATCTCTCC

T K A A C P T M G E A H N D K R A D P A
 2761 ACCAAGAGCTGCGTCCCCGACCATGGGAGAAGCTCACAATGACAAAGCTGCTGACCCAGCT

F V C R Q G V V D R G W G N G C G L F G
 2821 TTTGTGTGCAGACAGGAGTGGTGGACAGGGGCTGGGGCAACGGCTGCGGACTATTTGGC

K G S I D T C A K F A C S T K A I G R T
 2881 AAAGGAAGCATTGACACATGCGCCAAATTTGCCTGCTCTACCAAGGCAATAGGAAGAACC

mutated T5NT
 I L K E N I K Y E V A I F V H G P T T V
 2941 ATCTTGAAAGAGAATATCAAGTACGAAGTGGCCATCTTCGTGGACGGCACTACTGTG

E S H G N Y S T Q V G A T Q A G R F S I
 3001 GAGTCGCACGGAACTACTCCACACAGGTGGAGCCACTAGGCAAGGAGATTGAGCATC

T P A A P S Y T L K L G E Y G E V T V D
 3061 ACTCCCTGCGGGCCCTTCATACACACTAAAGCTTGGAGAATATGGAGAGGTGACAGTGGAC

C E P R S G I D T N A Y Y V M T V G T K
 3121 TGTGAACCAAGCTCAGGGATTGACACCAATGCATACTACGTGATGACTGTTGGAACAAGG

T F L V H R E W F M D L N L P W S S A G
 3181 ACGTTCTTTGGTCCATCGTGAGTGGTTCATGGACCTCAACCTCCCTTGGAGCAGTGCTGGA

S T V W R N R E T L M E F E E P H A T K
 3241 AGTACTGTGTGGAGGAACAGAGAGACGTTAATGGAGTTTGGAGAACACACGCCACGAAG

Q S V I A L G S Q E G A L H Q A L A G A
 3301 CAGTCTGTGATAGCATTTGGGCTCACAAGAGGGAGCTCTGCATCAAGCTTTGGCTGGAGCC

I P V E F S S N T V K L T S G H L K C R
 3361 ATTCCGTGTGAATTTTCAAGCAACACTGTCAAGTTGACGTGGGCTGATTGAAAGTGTAGA

V K M E K L Q L K G T T Y G V C S K A F
 3421 GTGAAGATGGAAAAATTGACAGTTGAAGGGAACAACCTATGGCGTCTGTTCAAGGCTTTTC

K F L G T P A D T G H G T V V L E L Q Y
 3481 AAGTTTCTTTGGGACTCCCGCAGACACAGGTACAGGCACCTGTGGTGTGGAATTGCACTAC

T G T D G P C K V P I S S A A S L N D L
 3541 ACTGGCACGGATGGACCTTGCAAAGTTCTATCTCGTCAGCGGCTTCATTGAACGACCTA

T P V G R L V T V N P F V S V A T A N A
 3601 ACGCCAGTGGGCAGATTGGTCACTGTCAACCCCTTTTGTTCAGTGCCACGGCCAACGCT

K V L I E L E P P F G D S Y I V V G R G
 3661 AAGGTCCTGATTGAATTGGAACCACCCCTTGGGAGACTCATCATAGTGGTGGGCAGAGGA

REPLACEMENT SHEET

Figure 9 continued

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3721      E Q Q I N H H W H K S G S S I G K A F T
      GAACAACAGATCAATCACCATTGGCACAAGTCTGGAAGCAGCATTGGCAAAGCCTTTACA

3781      T T L K G A Q R L A A L G D T A W D F G
      ACCACCCCTCAAAGGAGCGCAGAGACTAGCCGCTCTAGGAGACACAGCTTGGGACTTTGGA

3841      S V G G V F T S V G K A V H Q V F G G A
      TCAGTTGGAGGGGTGTTCCCTCAGTTGGGAAGGCTGTCCATCAAGTGTTCGGAGGAGCA

3901      F R S L F G G M S W I T Q G L L G A L L
      TTCGCTCACTGTTCCGAGGCATGTCCTGGATAACGCAAGGATTGCTGGGGGCTCTCCTG

3961      L W M G I N A R D R S I A L T F L A V G
      TTGTGGATGGGCATCAATGCTCGTGATAGGTCCATAGCTCTCACGTTTCTCGCAGTTGGA

                                                    => C5L

4021      G V L L F L S V N V H A *
      GGAGTTCTGCTCTTCCCTCTCCGTGAACGTGCACGCTTAATTTTTATCTAGAATCGATCCC

4081      GGGTTTTATGACTAGTTAATCACGGCCGCTTATAAGATCTAAATGSCATAATTTCTAA

4141      ATAATGAAAAAAGTACATCATGAGCAACGCGTTAGTATATTTTACAATGGAGATTAAAG

4201      CTCTATACCGTTCTATGTTTATTGATTCAGATGATGTTTTAGAAAAGAAAGTTATTGAAT

4261      ATGAAAACTTTAAATGAAGATGAAGATGACGACGATGATTATTGTTGTAATCTCGTTTAG

4321      ATGAAGAAGATGACGCGCTAAAGTATACTATGGTTACAAAGTATAAGTCTATACTACTAA

4381      TGGCGACTTGTGCAAGAAAGTATAGTATAGTGAATAATGTTGTAGATTATGATTATGAA

4441      AACCAATTAATCAGATCCATATCTAAAGGTATCTCCCTTTCGACATAATTTTCATCTATTTC

4501      CTAGTTTGAATAACCTGCAGCCAAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACT

4561      GGGAAAACCCCTGGCGTTACCCAACCTAATCGCCTTGCAACATCCCCCTTTCGCCAGCT

4621      GGCCTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATG

4681      GCGAATGGCGCCTGATCGGTTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCA

4741      TATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGATAGTTAAGCCAGCCCCGACACC

4801      CGCCAACACCCGCTGACGCGCCCTGACGGGCTGTGCTGCTCCCGGCATCCGCTTACAGAC

4861      AAGCTGTGACCGTCTCCGGAGCTGCATGTGTGTCAGAGGTTTTACCGCTCATACCGGAAAC

4921      GCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAA

4981      TGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTGTGT

5041      TATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCGTGATAAATGC

5101      TTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCACATTTCCTGTGCGCCCTTATTTC

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REPLACEMENT SHEET

Figure 9 continued

5161 CCTTTTTCGCGCATTTTGCCCTCCTGTTTTTGTCTACCCAGAAACGCTGGTGAAAGTAA
5221 AAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTACATCGAATCGGATCTCAACAGCG
5281 GTAAGATCCTTGAGAGTTTTTCGCCCGAAGAAGCTTTTCCAATGATGAGCACTTTTAAAG
5341 TTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTGCGC
5401 GCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTA
5461 CGGATGGCATGACAGTAAGAGAAATTATGCAGTGTGCCATAAACCATGAGTGATAAACA
5521 CGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACA
5581 ACATGGGGGATCATGTAACTCGCCCTTGATCGTTGGGAACCGAGCTGAATGAAGCCATAC
5641 CAAACGACGAGCGTGACACCAGATGCCCTGTAGCAATGGCAACAACGTTGCGCAAACTAT
5701 TAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGG
5761 ATAAAGTTGACAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATA
5821 AATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTCGACGACTGGGGCCAGATGGTA
5881 AGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAA
5941 ATAGACAGATCGCTGAGATAGTGCCTCACTGATTAAGCATTTGGTAACGTGACAGCAAG
6001 TTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTTAATTTAAAGGATCTAGG
6061 TGAAGATCCTTTTGTATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACT
6121 GAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCG
6181 TAATCTGCTGCTTGCAAAACAAAAAACCCCGCTACCAGCGGTGGTTGTTTGGCCGGATC
6241 AAGAGCTACCACTCTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATACCAATA
6301 CTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACCTTCAAGAACTCTGTAGACCCGCTA
6361 CATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTC
6421 TTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTGCGGCTGAACGG
6481 GGGGTTTCGTGCACACAGCCAGCTTGAGAGCAACGACCTACACCGAACTGAGATACCTAC
6541 AGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGG
6601 TAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGAGCTTCCAGGGGAAACGCCCTGGT
6661 ATCTTTATAGTCCGTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCT
6721 CGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCTGG
6781 CCTTTGCTGGCCTTTGCTCACATGTTCTTCTCGCTTATCCCTGATTCGTGGATA

REPLACEMENT SHEET

Figure 9 continued

6841 ACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCA
6901 GCGAGTCAGTGAGCGAGGAAGCGGAAGA

REPLACEMENT SHEET

FIGURE 12

agtagttcgc ctgtgtgagc tgacaaactt agtagtggtt gtgaggatta acaacaatta
60

acacagtgcg agctgtttct tagcacgaag atctcg atg tct aag aaa cca gga
114

Met Ser Lys Lys Pro Gly
1 5

ggg ccc ggc aag agc cgg gct gtc aat atg cta aaa cgc gga atg ccc
162

Gly Pro Gly Lys Ser Arg Ala Val Asn Met Leu Lys Arg Gly Met Pro
10 15 20

cgc gtg ttg tcc ttg att gga ctg aag agg gct atg ttg agc ctg atc
210

Arg Val Leu Ser Leu Ile Gly Leu Lys Arg Ala Met Leu Ser Leu Ile
25 30 35

gac ggc aag ggg cca ata cga ttt gtg ttg gct ctc ttg gcg ttc ttc
258

Asp Gly Lys Gly Pro Ile Arg Phe Val Leu Ala Leu Leu Ala Phe Phe
40 45 50

agg ttc aca gca att gct ccg acc cga gca gtg ctg gat cga tgg aga
306

Arg Phe Thr Ala Ile Ala Pro Thr Arg Ala Val Leu Asp Arg Trp Arg
55 60 65 70

ggt gtg aac aaa caa aca gcg atg aaa cac ctt ctg agt ttt aag aag
354

Gly Val Asn Lys Gln Thr Ala Met Lys His Leu Leu Ser Phe Lys Lys
75 80 85

gaa cta ggc acc ttg acc agt gct atc aat cgg cgg agc tca aaa caa
402

Glu Leu Gly Thr Leu Thr Ser Ala Ile Asn Arg Arg Ser Ser Lys Gln
90 95 100

aag aaa aga gga gga aag acc gga att gca gtc atg att ggc ctg atc
450

Lys Lys Arg Gly Gly Lys Thr Gly Ile Ala Val Met Ile Gly Leu Ile
105 110 115

gcc agc gta gga gca gtt acc ctc tct aac ttc caa ggg aag gtg atg
498

Ala Ser Val Gly Ala Val Thr Leu Ser Asn Phe Gln Gly Lys Val Met
120 125 130

REPLACEMENT SHEET

Figure 12 continued

atg acg gta aat gct act gac gtc aca gat gtc atc acg att cca aca
546

Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr Ile Pro Thr
135 140 145 150

gct gct gga aag aac cta tgc att gtc aga gca atg gat gtg gga tac
594

Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp Val Gly Tyr
155 160 165

atg tgc gat gat act atc act tat gaa tgc cca gtg ctg tcg gct ggt
642

Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu Ser Ala Gly
170 175 180

aat gat cca gaa gac atc gac tgt tgg tgc aca aag tca gca gtc tac
690

Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser Ala Val Tyr
185 190 195

gtc agg tat gga aga tgc acc aag aca cgc cac tca aga cgc agt cgg
738

Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg Arg Ser Arg
200 205 210

agg tca ctg aca gtg cag aca cac gga gaa agc act cta gcg aac aag
786

Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu Ala Asn Lys
215 220 225 230

aag ggg gct tgg atg gac agc acc aag gcc aca agg tat ttg gta aaa
834

Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr Leu Val Lys
235 240 245

aca gaa tca tgg atc ttg agg aac cct gga tat gcc ctg gtg gca gcc
882

Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu Val Ala Ala
250 255 260

gtc att ggt tgg atg ctt ggg agc aac acc atg cag aga gtt gtg ttt
930

Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg Val Val Phe
265 270 275

gtc gtg cta ttg ctt ttg gtg gcc cca gct tac agc ttc aac tgc ctt
978

Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu
280 285 290

REPLACEMENT SHEET

Figure 12 continued

gga atg agc aac aga gac ttc ttg gaa gga gtg tct gga gca aca tgg
1026

Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly Ala Thr Trp
295 300 305 310

gtg gat ttg gtt ctc gaa ggc gac agc tgc gtg act atc atg tct aag
1074

Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile Met Ser Lys
315 320 325

gac aag cct acc atc gat gtg aag atg atg aat atg gag gcg gcc aac
1122

Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu Ala Ala Asn
330 335 340

ctg gca gag gtc cgc agt tat tgc tat ttg gct acc gtc agc gat ctc
1170

Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val Ser Asp Leu
345 350 355

tcc acc aaa gct gcg tgc ccg acc atg gga gaa gct cac aat gac aaa
1218

Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His Asn Asp Lys
360 365 370

cgt gct gac cca gct ttt gtg tgc aga caa gga gtg gtg gac agg ggc
1266

Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val Asp Arg Gly
375 380 385 390

tggtggc aac ggc tgc gga cta ttt ggc aaa gga agc att gac aca tgc
1314

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys
395 400 405

gcc aaa ttt gcc tgc tct acc aag gca ata gga aga acc atc ttg aaa
1362

Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr Ile Leu Lys
410 415 420

gag aat atc aag tac gaa gtg gcc att ttt gtc cat gga cca act act
1410

Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly Pro Thr Thr
425 430 435

gtg gag tcg cac gga aac tac tcc aca cag gtt gga gcc act cag gca
1458

Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala Thr Gln Ala
440 445 450

REPLACEMENT SHEET

Figure 12 continued

ggg aga ttc agc atc act cct gcg gcg cct tca tac aca cta aag ctt
1506

Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr Leu Lys Leu
455 460 465 470

gga gaa tat gga gag gtg aca gtg gac tgt gaa cca cgg tca ggg att
1554

Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg Ser Gly Ile
475 480 485

gac acc aat gca tac tac gtg atg act gtt gga aca aag acg ttc ttg
1602

Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys Thr Phe Leu
490 495 500

gtc cat cgt gag tgg ttc atg gac ctc aac ctc cct tgg agc agt gct
1650

Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp Ser Ser Ala
505 510 515

gga agt act gtg tgg agg aac aga gag acg tta atg gag ttt gag gaa
1698

Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu Phe Glu Glu
520 525 530

cca cac gcc acg aag cag tct gtg ata gca ttg ggc tca caa gag gga
1746

Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser Gln Glu Gly
535 540 545 550

gct ctg cat caa gct ttg gct gga gcc att cct gtg gaa ttt tca agc
1794

Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu Phe Ser Ser
555 560 565

aac act gtc aag ttg acg tcg ggt cat ttg aag tgt aga gtg aag atg
1842

Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg Val Lys Met
570 575 580

gaa aaa ttg cag ttg aag gga aca acc tat ggc gtc tgt tca aag gct
1890

Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys Ser Lys Ala
585 590 595

ttc aag ttt ctt ggg act ccc gca gac aca ggt cac ggc act gtg gtg
1938

Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly Thr Val Val
600 605 610

REPLACEMENT SHEET

Figure 12 continued

ttg gaa ttg cag tac act ggc acg gat gga cct tgc aaa gtt cct atc
1986

Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys Val Pro Ile
615 620 625 630

tcg tca gtg gct tca ttg aac gac cta acg cca gtg ggc aga ttg gtc
2034

Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly Arg Leu Val
635 640 645

act gtc aac cct ttt gtt tca gtg gcc acg gcc aac gct aag gtc ctg
2082

Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala Lys Val Leu
650 655 660

att gaa ttg gaa cca ccc ttt gga gac tca tac ata gtg gtg ggc aga
2130

Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg
665 670 675

gga gaa caa cag atc aat cac cat tgg cac aag tct gga agc agc att
2178

Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly Ser Ser Ile
680 685 690

ggc aaa gcc ttt aca acc acc ctc aaa gga gcg cag aga cta gcc gct
2226

Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala
695 700 705 710

cta gga gac aca gct tgg gac ttt gga tca gtt gga ggg gtg ttc acc
2274

Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Val Phe Thr
715 720 725

tca gtt ggg aag gct gtc cat caa gtg ttc gga gga gca ttc cgc tca
2322

Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Ser
730 735 740

ctg ttc gga ggc atg tcc tgg ata acg caa gga ttg ctg ggg gct ctc
2370

Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu Gly Ala Leu
745 750 755

ctg ttg tgg atg ggc atc aat gct cgt gat agg tcc ata gct ctc acg
2418

Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile Ala Leu Thr
760 765 770

REPLACEMENT SHEET

Figure 12 continued

ttt ctc gca gtt gga gga gtt ctg ctc ttc ctc tcc gtg aac gtg cac
2466

Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val Asn Val His
775 780 785 790

gct gac act ggg tgt gcc ata gac atc agc cgg caa gag ctg aga tgt
2514

Ala Asp Thr Gly Cys Ala Ile Asp Ile Ser Arg Gln Glu Leu Arg Cys
795 800 805

gga agt gga gtg ttc ata cac aat gat gtg gag gct tgg atg gac cgg
2562

Gly Ser Gly Val Phe Ile His Asn Asp Val Glu Ala Trp Met Asp Arg
810 815 820

tac aag tat tac cct gaa acg cca caa ggc cta gcc aag atc att cag
2610

Tyr Lys Tyr Tyr Pro Glu Thr Pro Gln Gly Leu Ala Lys Ile Ile Gln
825 830 835

aaa gct cat aag gaa gga gtg tgc ggt cta cga tca gtt tcc aga ctg
2658

Lys Ala His Lys Glu Gly Val Cys Gly Leu Arg Ser Val Ser Arg Leu
840 845 850

gag cat caa atg tgg gaa gca gtg aag gac gag ctg aac act ctt ttg
2706

Glu His Gln Met Trp Glu Ala Val Lys Asp Glu Leu Asn Thr Leu Leu
855 860 865 870

aag gag aat ggt gtg gac ctt agt gtc gtg gtt gag aaa cag gag gga
2754

Lys Glu Asn Gly Val Asp Leu Ser Val Val Val Glu Lys Gln Glu Gly
875 880 885

atg tac aag tca gca cct aaa cgc ctc acc gcc acc acg gaa aaa ttg
2802

Met Tyr Lys Ser Ala Pro Lys Arg Leu Thr Ala Thr Thr Glu Lys Leu
890 895 900

gaa att ggc tgg aag gcc tgg gga aag agt att tta ttt gca cca gaa
2850

Glu Ile Gly Trp Lys Ala Trp Gly Lys Ser Ile Leu Phe Ala Pro Glu
905 910 915

ctc gcc aac aac acc ttt gtg gtt gat ggt ccg gag acc aag gaa tgt
2898

Leu Ala Asn Asn Thr Phe Val Val Asp Gly Pro Glu Thr Lys Glu Cys
920 925 930

REPLACEMENT SHEET

Figure 12 continued

ccg act cag aat cgc gct tgg aat agc tta gaa gtg gag gat ttt gga
2946

Pro Thr Gln Asn Arg Ala Trp Asn Ser Leu Glu Val Glu Asp Phe Gly
935 940 945 950

ttt ggt ctc acc agc act cgg atg ttc ctg aag gtc aga gag agc aac
2994

Phe Gly Leu Thr Ser Thr Arg Met Phe Leu Lys Val Arg Glu Ser Asn
955 960 965

aca act gaa tgt gac tcg aag atc att gga acg gct gtc aag aac aac
3042

Thr Thr Glu Cys Asp Ser Lys Ile Ile Gly Thr Ala Val Lys Asn Asn
970 975 980

ttg gcg atc cac agt gac ctg tcc tat tgg att gaa agc agg ctc aat
3090

Leu Ala Ile His Ser Asp Leu Ser Tyr Trp Ile Glu Ser Arg Leu Asn
985 990 995

gat acg tgg aag ctt gaa agg gca gtt ctg ggt gaa gtc aaa tca
3135

Asp Thr Trp Lys Leu Glu Arg Ala Val Leu Gly Glu Val Lys Ser
1000 1005 1010

tgt acg tgg cct gag acg cat acc ttg tgg ggc gat gga atc ctt
3180

Cys Thr Trp Pro Glu Thr His Thr Leu Trp Gly Asp Gly Ile Leu
1015 1020 1025

gag agt gac ttg ata ata cca gtc aca ctg gcg gga cca cga agc
3225

Glu Ser Asp Leu Ile Ile Pro Val Thr Leu Ala Gly Pro Arg Ser
1030 1035 1040

aat cac aat cgg aga cct ggg tac aag aca caa aac cag ggc cca
3270

Asn His Asn Arg Arg Pro Gly Tyr Lys Thr Gln Asn Gln Gly Pro
1045 1050 1055

tgg gac gaa ggc cgg gta gag att gac ttc gat tac tgc cca gga
3315

Trp Asp Glu Gly Arg Val Glu Ile Asp Phe Asp Tyr Cys Pro Gly
1060 1065 1070

act acg gtc acc ctg agt gag agc tgc gga cac cgt gga cct gcc
3360

Thr Thr Val Thr Leu Ser Glu Ser Cys Gly His Arg Gly Pro Ala
1075 1080 1085

REPLACEMENT SHEET

Figure 12 continued

act cgc	acc acc aca gag agc	gga aag ttg ata aca	gat tgg tgc
3405			
Thr Arg	Thr Thr Thr Glu Ser	Gly Lys Leu Ile Thr	Asp Trp Cys
1090	1095	1100	
tgc agg	agc tgc acc tta cca	cca ctg cgc tac caa	act gac agc
3450			
Cys Arg	Ser Cys Thr Leu Pro	Pro Leu Arg Tyr Gln	Thr Asp Ser
1105	1110	1115	
ggc tgt	tgg tat ggt atg gag	atc aga cca cag aga	cat gat gaa
3495			
Gly Cys	Trp Tyr Gly Met Glu	Ile Arg Pro Gln Arg	His Asp Glu
1120	1125	1130	
aag acc	ctc gtg cag tca caa	gtg aat gct tat aat	gct gat atg
3540			
Lys Thr	Leu Val Gln Ser Gln	Val Asn Ala Tyr Asn	Ala Asp Met
1135	1140	1145	
att gac	cct ttt cag ttg ggc	ctt ctg gtc gtg ttc	ttg gcc acc
3585			
Ile Asp	Pro Phe Gln Leu Gly	Leu Leu Val Val Phe	Leu Ala Thr
1150	1155	1160	
cag gag	gtc ctt cgc aag agg	tgg aca gcc aag atc	agc atg cca
3630			
Gln Glu	Val Leu Arg Lys Arg	Trp Thr Ala Lys Ile	Ser Met Pro
1165	1170	1175	
gct ata	ctg att gct ctg cta	gtc ctg gtg ttt ggg	ggc att act
3675			
Ala Ile	Leu Ile Ala Leu Leu	Val Leu Val Phe Gly	Gly Ile Thr
1180	1185	1190	
tac act	gat gtg tta cgc tat	gtc atc ttg gtg ggg	gca gct ttc
3720			
Tyr Thr	Asp Val Leu Arg Tyr	Val Ile Leu Val Gly	Ala Ala Phe
1195	1200	1205	
gca gaa	tct aat tcg gga gga	gac gtg gta cac ttg	gcg ctc atg
3765			
Ala Glu	Ser Asn Ser Gly Gly	Asp Val Val His Leu	Ala Leu Met
1210	1215	1220	
gcg acc	ttc aag ata caa cca	gtg ttt atg gtg gca	tcg ttt ctc
3810			
Ala Thr	Phe Lys Ile Gln Pro	Val Phe Met Val Ala	Ser Phe Leu
1225	1230	1235	

REPLACEMENT SHEET

Figure 12 continued

aaa gcg 3855	aga tgg acc aac cag	gag aac att ttg ttg	atg ttg gcg
Lys Ala 1240	Arg Trp Thr Asn Gln	Glu Asn Ile Leu Leu	Met Leu Ala 1250
gct gtt 3900	ttc ttt caa atg gct	tat cac gat gcc cgc	caa att ctg
Ala Val 1255	Phe Phe Gln Met Ala	Tyr His Asp Ala Arg	Gln Ile Leu 1265
ctc tgg 3945	gag atc cct gat gtg	ttg aat tca ctg gcg	gta gct tgg
Leu Trp 1270	Glu Ile Pro Asp Val	Leu Asn Ser Leu Ala	Val Ala Trp 1280
atg ata 3990	ctg aga gcc ata aca	ttc aca acg aca tca	aac gtg gtt
Met Ile 1285	Leu Arg Ala Ile Thr	Phe Thr Thr Thr Ser	Asn Val Val 1295
gtt ccg 4035	ctg cta gcc ctg cta	aca ccc ggg ctg aga	tgc ttg aat
Val Pro 1300	Leu Leu Ala Leu Leu	Thr Pro Gly Leu Arg	Cys Leu Asn 1310
ctg gat 4080	gtg tac agg ata ctg	ctg ttg atg gtc gga	ata ggc agc
Leu Asp 1315	Val Tyr Arg Ile Leu	Leu Leu Met Val Gly	Ile Gly Ser 1325
ttg atc 4125	agg gag aag agg agt	gca gct gca aaa aag	aaa gga gca
Leu Ile 1330	Arg Glu Lys Arg Ser	Ala Ala Ala Lys Lys	Lys Gly Ala 1340
agt ctg 4170	cta tgc ttg gct cta	gcc tca aca gga ctt	ttc aac ccc
Ser Leu 1345	Leu Cys Leu Ala Leu	Ala Ser Thr Gly Leu	Phe Asn Pro 1355
atg atc 4215	ctt gct gct gga ctg	att gca tgt gat ccc	aac cgt aaa
Met Ile 1360	Leu Ala Ala Gly Leu	Ile Ala Cys Asp Pro	Asn Arg Lys 1370
cgc gga 4260	tgg ccc gca act gaa	gtg atg aca gct gtc	ggc cta atg
Arg Gly 1375	Trp Pro Ala Thr Glu	Val Met Thr Ala Val	Gly Leu Met 1385

REPLACEMENT SHEET

Figure 12 continued

ttt gcc 4305	atc gtc gga ggg ctg	gca gag ctt gac att	gac tcc atg
Phe Ala 1390	Ile Val Gly Gly Leu	Ala Glu Leu Asp Ile	Asp Ser Met 1400
gcc att 4350	cca atg act atc gcg	ggg ctc atg ttt gct	gct ttc gtg
Ala Ile 1405	Pro Met Thr Ile Ala	Gly Leu Met Phe Ala	Ala Phe Val 1415
att tct 4395	ggg aaa tca aca gat	atg tgg att gag aga	acg gcg gac
Ile Ser 1420	Gly Lys Ser Thr Asp	Met Trp Ile Glu Arg	Thr Ala Asp 1430
att tcc 4440	tgg gaa agt gat gca	gaa att aca ggc tcg	agc gaa aga
Ile Ser 1435	Trp Glu Ser Asp Ala	Glu Ile Thr Gly Ser	Ser Glu Arg 1445
gtt gat 4485	gtg cgg ctt gat gat	gat gga aac ttc cag	ctc atg aat
Val Asp 1450	Val Arg Leu Asp Asp	Asp Gly Asn Phe Gln	Leu Met Asn 1460
gat cca 4530	gga gca cct tgg aag	ata tgg atg ctc aga	atg gtc tgt
Asp Pro 1465	Gly Ala Pro Trp Lys	Ile Trp Met Leu Arg	Met Val Cys 1475
ctc gcg 4575	att agt gcg tac acc	ccc tgg gca atc ttg	ccc tca gta
Leu Ala 1480	Ile Ser Ala Tyr Thr	Pro Trp Ala Ile Leu	Pro Ser Val 1490
gtt gga 4620	ttt tgg ata act ctc	caa tac aca aag aga	gga ggc gtg
Val Gly 1495	Phe Trp Ile Thr Leu	Gln Tyr Thr Lys Arg	Gly Gly Val 1505
ttg tgg 4665	gac act ccc tca cca	aag gag tac aaa aag	ggg gac acg
Leu Trp 1510	Asp Thr Pro Ser Pro	Lys Glu Tyr Lys Lys	Gly Asp Thr 1520
acc acc 4710	ggc gtc tac agg atc	atg act cgt ggg ctg	ctc ggc agt
Thr Thr 1525	Gly Val Tyr Arg Ile	Met Thr Arg Gly Leu	Leu Gly Ser 1535

REPLACEMENT SHEET

Figure 12 continued

tat caa 4755	gca gga gcg ggc gtg	atg gtt gaa ggt gtt	ttc cac acc
Tyr Gln 1540	Ala Gly Ala Gly Val 1545	Met Val Glu Gly Val 1550	Phe His Thr
ctt tgg 4800	cat aca aca aaa gga	gcc gct ttg atg agc	gga gag ggc
Leu Trp 1555	His Thr Thr Lys Gly 1560	Ala Ala Leu Met Ser 1565	Gly Glu Gly
cgc ctg 4845	gac cca tac tgg ggc	agt gtc aag gag gat	cga ctt tgt
Arg Leu 1570	Asp Pro Tyr Trp Gly 1575	Ser Val Lys Glu Asp 1580	Arg Leu Cys
tac gga 4890	gga ccc tgg aaa ttg	cag cac aag tgg aac	ggg cag gat
Tyr Gly 1585	Gly Pro Trp Lys Leu 1590	Gln His Lys Trp Asn 1595	Gly Gln Asp
gag gtg 4935	cag atg att gtg gtg	gaa cct ggc aag aac	gtt aag aac
Glu Val 1600	Gln Met Ile Val Val 1605	Glu Pro Gly Lys Asn 1610	Val Lys Asn
gtc cag 4980	acg aaa cca ggg gtg	ttc aaa aca cct gaa	gga gaa atc
Val Gln 1615	Thr Lys Pro Gly Val 1620	Phe Lys Thr Pro Glu 1625	Gly Glu Ile
ggg gcc 5025	gtg act ttg gac ttc	ccc act gga aca tca	ggc tca cca
Gly Ala 1630	Val Thr Leu Asp Phe 1635	Pro Thr Gly Thr Ser 1640	Gly Ser Pro
ata gtg 5070	gac aaa aac ggt gat	gtg att ggg ctt tat	ggc aat gga
Ile Val 1645	Asp Lys Asn Gly Asp 1650	Val Ile Gly Leu Tyr 1655	Gly Asn Gly
gtc ata 5115	atg ccc aac ggc tca	tac ata agc gcg ata	gtg cag ggt
Val Ile 1660	Met Pro Asn Gly Ser 1665	Tyr Ile Ser Ala Ile 1670	Val Gln Gly
gaa agg 5160	atg gat gag cca atc	cca gcc gga ttc gaa	cct gag atg
Glu Arg 1675	Met Asp Glu Pro Ile 1680	Pro Ala Gly Phe Glu 1685	Pro Glu Met

REPLACEMENT SHEET

Figure 12 continued

ctg agg	aaa aaa cag atc act	gta ctg gat ctc cat	ccc ggc gcc
5205			
Leu Arg	Lys Lys Gln Ile Thr	Val Leu Asp Leu His	Pro Gly Ala
1690	1695	1700	
ggt aaa	aca agg agg att ctg	cca cag atc atc aaa	gag gcc ata
5250			
Gly Lys	Thr Arg Arg Ile Leu	Pro Gln Ile Ile Lys	Glu Ala Ile
1705	1710	1715	
aac aga	aga ctg aga aca gcc	gtg cta gca cca acc	agg gtt gtg
5295			
Asn Arg	Arg Leu Arg Thr Ala	Val Leu Ala Pro Thr	Arg Val Val
1720	1725	1730	
gct gct	gag atg gct gaa gca	ctg aga gga ctg ccc	atc cgg tac
5340			
Ala Ala	Glu Met Ala Glu Ala	Leu Arg Gly Leu Pro	Ile Arg Tyr
1735	1740	1745	
cag aca	tcc gca gtg ccc aga	gaa cat aat gga aat	gag att gtt
5385			
Gln Thr	Ser Ala Val Pro Arg	Glu His Asn Gly Asn	Glu Ile Val
1750	1755	1760	
gat gtc	atg tgt cat gct acc	ctc acc cac agg ctg	atg tct cct
5430			
Asp Val	Met Cys His Ala Thr	Leu Thr His Arg Leu	Met Ser Pro
1765	1770	1775	
cac agg	gtg ccg aac tac aac	ctg ttc gtg atg gat	gag gct cat
5475			
His Arg	Val Pro Asn Tyr Asn	Leu Phe Val Met Asp	Glu Ala His
1780	1785	1790	
ttc acc	gac cca gct agc att	gca gca aga ggt tac	att tcc aca
5520			
Phe Thr	Asp Pro Ala Ser Ile	Ala Ala Arg Gly Tyr	Ile Ser Thr
1795	1800	1805	
aag gtc	gag cta ggg gag gcg	gcg gca ata ttc atg	aca gcc acc
5565			
Lys Val	Glu Leu Gly Glu Ala	Ala Ala Ile Phe Met	Thr Ala Thr
1810	1815	1820	
cca cca	ggc act tca gat cca	ttc cca gag tcc aat	tca cca att
5610			
Pro Pro	Gly Thr Ser Asp Pro	Phe Pro Glu Ser Asn	Ser Pro Ile
1825	1830	1835	

REPLACEMENT SHEET

Figure 12 continued

tcc gac	tta cag act gag atc	ccg gat cga gct tgg	aac tct gga
5655			
Ser Asp	Leu Gln Thr Glu Ile	Pro Asp Arg Ala Trp	Asn Ser Gly
1840	1845	1850	
tac gaa	tgg atc aca gaa tac	acc ggg aag acg gtt	tgg ttt gtg
5700			
Tyr Glu	Trp Ile Thr Glu Tyr	Thr Gly Lys Thr Val	Trp Phe Val
1855	1860	1865	
cct agt	gtc aag atg ggg aat	gag att gcc ctt tgc	cta caa cgt
5745			
Pro Ser	Val Lys Met Gly Asn	Glu Ile Ala Leu Cys	Leu Gln Arg
1870	1875	1880	
gct gga	aag aaa gta gtc caa	ttg aac aga aag tcg	tac gag acg
5790			
Ala Gly	Lys Lys Val Val Gln	Leu Asn Arg Lys Ser	Tyr Glu Thr
1885	1890	1895	
gag tac	cca aaa tgt aag aac	gat gat tgg gac ttt	gtt atc aca
5835			
Glu Tyr	Pro Lys Cys Lys Asn	Asp Asp Trp Asp Phe	Val Ile Thr
1900	1905	1910	
aca gac	ata tct gaa atg ggg	gct aac ttc aag gcg	agc agg gtg
5880			
Thr Asp	Ile Ser Glu Met Gly	Ala Asn Phe Lys Ala	Ser Arg Val
1915	1920	1925	
att gac	agc cgg aag agt gtg	aaa cca acc atc ata	aca gaa gga
5925			
Ile Asp	Ser Arg Lys Ser Val	Lys Pro Thr Ile Ile	Thr Glu Gly
1930	1935	1940	
gaa ggg	aga gtg atc ctg gga	gaa cca tct gca gtg	aca gca gct
5970			
Glu Gly	Arg Val Ile Leu Gly	Glu Pro Ser Ala Val	Thr Ala Ala
1945	1950	1955	
agt gcc	gcc cag aga cgt gga	cgt atc ggt aga aat	ccg tcg caa
6015			
Ser Ala	Ala Gln Arg Arg Gly	Arg Ile Gly Arg Asn	Pro Ser Gln
1960	1965	1970	
gtt ggt	gat gag tac tgt tat	ggg ggg cac acg aat	gaa gac gac
6060			
Val Gly	Asp Glu Tyr Cys Tyr	Gly Gly His Thr Asn	Glu Asp Asp
1975	1980	1985	

REPLACEMENT SHEET

Figure 12 continued

tcg aac 6105	ttc gcc cat tgg act	gag gca cga atc atg	ctg gac aac
Ser Asn 1990	Phe Ala His Trp Thr 1995	Glu Ala Arg Ile Met 2000	Leu Asp Asn
atc aac 6150	atg cca aac gga ctg	atc gct caa ttc tac	caa cca gag
Ile Asn 2005	Met Pro Asn Gly Leu 2010	Ile Ala Gln Phe Tyr 2015	Gln Pro Glu
cgt gag 6195	aag gta tat acc atg	gat ggg gaa tac cgg	ctc aga gga
Arg Glu 2020	Lys Val Tyr Thr Met 2025	Asp Gly Glu Tyr Arg 2030	Leu Arg Gly
gaa gag 6240	aga aaa aac ttt ctg	gaa ctg ttg agg act	gca gat ctg
Glu Glu 2035	Arg Lys Asn Phe Leu 2040	Glu Leu Leu Arg Thr 2045	Ala Asp Leu
cca gtt 6285	tgg ctg gct tac aag	gtt gca gcg gct gga	gtg tca tac
Pro Val 2050	Trp Leu Ala Tyr Lys 2055	Val Ala Ala Ala Gly 2060	Val Ser Tyr
cac gac 6330	cgg agg tgg tgc ttt	gat ggt cct agg aca	aac aca att
His Asp 2065	Arg Arg Trp Cys Phe 2070	Asp Gly Pro Arg Thr 2075	Asn Thr Ile
tta gaa 6375	gac aac aac gaa gtg	gaa gtc atc acg aag	ctt ggt gaa
Leu Glu 2080	Asp Asn Asn Glu Val 2085	Glu Val Ile Thr Lys 2090	Leu Gly Glu
agg aag 6420	att ctg agg ccg cgc	tgg att gac gcc agg	gtg tac tcg
Arg Lys 2095	Ile Leu Arg Pro Arg 2100	Trp Ile Asp Ala Arg 2105	Val Tyr Ser
gat cac 6465	cag gca cta aag gcg	ttc aag gac ttc gcc	tcg gga aaa
Asp His 2110	Gln Ala Leu Lys Ala 2115	Phe Lys Asp Phe Ala 2120	Ser Gly Lys
cgt tct 6510	cag ata ggg ctc att	gag gtt ctg gga aag	atg cct gag
Arg Ser 2125	Gln Ile Gly Leu Ile 2130	Glu Val Leu Gly Lys 2135	Met Pro Glu

REPLACEMENT SHEET

Figure 12 continued

cac ttc 6555	atg ggg aag aca tgg	gaa gca ctt gac acc	atg tac gtt
His Phe 2140	Met Gly Lys Thr Trp 2145	Glu Ala Leu Asp Thr 2150	Met Tyr Val
gtg gcc 6600	act gca gag aaa gga	gga aga gct cac aga	atg gcc ctg
Val Ala 2155	Thr Ala Glu Lys Gly 2160	Gly Arg Ala His Arg 2165	Met Ala Leu
gag gaa 6645	ctg cca gat gct ctt	cag aca att gcc ttg	att gcc tta
Glu Glu 2170	Leu Pro Asp Ala Leu 2175	Gln Thr Ile Ala Leu 2180	Ile Ala Leu
ttg agt 6690	gtg atg acc atg gga	gta ttc ttc ctc ctc	atg cag cgg
Leu Ser 2185	Val Met Thr Met Gly 2190	Val Phe Phe Leu Leu 2195	Met Gln Arg
aag ggc 6735	att gga aag ata ggt	ttg gga ggc gct gtc	ttg gga gtc
Lys Gly 2200	Ile Gly Lys Ile Gly 2205	Leu Gly Gly Ala Val 2210	Leu Gly Val
gcg acc 6780	ttt ttc tgt tgg atg	gct gaa gtt cca gga	acg aag atc
Ala Thr 2215	Phe Phe Cys Trp Met 2220	Ala Glu Val Pro Gly 2225	Thr Lys Ile
gcc gga 6825	atg ttg ctg ctc tcc	ctt ctc ttg atg att	gtg cta att
Ala Gly 2230	Met Leu Leu Leu Ser 2235	Leu Leu Leu Met Ile 2240	Val Leu Ile
cct gag 6870	cca gag aag caa cgt	tcg cag aca gac aac	cag cta gcc
Pro Glu 2245	Pro Glu Lys Gln Arg 2250	Ser Gln Thr Asp Asn 2255	Gln Leu Ala
gtg ttc 6915	ctg att tgt gtc atg	acc ctt gtg agc gca	gtg gca gcc
Val Phe 2260	Leu Ile Cys Val Met 2265	Thr Leu Val Ser Ala 2270	Val Ala Ala
aac gag 6960	atg ggt tgg cta gat	aag acc aag agt gac	ata agc agt
Asn Glu 2275	Met Gly Trp Leu Asp 2280	Lys Thr Lys Ser Asp 2285	Ile Ser Ser

REPLACEMENT SHEET

Figure 12 continued

ttg ttt 7005	ggg caa aga att gag	gtc aag gag aat ttc	agc atg gga
Leu Phe 2290	Gly Gln Arg Ile 2295	Val Lys Glu Asn Phe 2300	Ser Met Gly
gag ttt 7050	ctt ttg gac ttg agg	ccg gca aca gcc tgg	tca ctg tac
Glu Phe 2305	Leu Leu Asp Leu 2310	Pro Ala Thr Ala Trp 2315	Ser Leu Tyr
gct gtg 7095	aca aca gcg gtc ctc	act cca ctg cta aag	cat ttg atc
Ala Val 2320	Thr Thr Ala Val 2325	Thr Pro Leu Leu Lys 2330	His Leu Ile
acg tca 7140	gat tac atc aac acc	tca ttg acc tca ata	aac gtt cag
Thr Ser 2335	Asp Tyr Ile Asn Thr 2340	Ser Leu Thr Ser Ile 2345	Asn Val Gln
gca agt 7185	gca cta ttc aca ctc	gcg cga ggc ttc ccc	ttc gtc gat
Ala Ser 2350	Ala Leu Phe Thr 2355	Ala Arg Gly Phe Pro 2360	Phe Val Asp
gtt gga 7230	gtg tcg gct ctc ctg	cta gca gcc gga tgc	tgg gga caa
Val Gly 2365	Val Ser Ala Leu 2370	Leu Ala Ala Gly Cys 2375	Trp Gly Gln
gtc acc 7275	ctc acc gtt acg gta	aca gcg gca aca ctc	ctt ttt tgc
Val Thr 2380	Leu Thr Val Thr 2385	Thr Ala Ala Thr Leu 2390	Leu Phe Cys
cac tat 7320	gcc tac atg gtt ccc	ggc tgg caa gct gag	gca atg cgc
His Tyr 2395	Ala Tyr Met Val 2400	Gly Trp Gln Ala Glu 2405	Ala Met Arg
tca gcc 7365	cag cgg cgg aca gcg	gcc gga atc atg aag	aac gct gta
Ser Ala 2410	Gln Arg Arg Thr 2415	Ala Gly Ile Met Lys 2420	Asn Ala Val
gtg gat 7410	ggc atc gtg gcc acg	gac gtc cca gaa tta	gag cgc acc
Val Asp 2425	Gly Ile Val Ala Thr 2430	Asp Val Pro Glu Leu 2435	Glu Arg Thr

REPLACEMENT SHEET

Figure 12 continued

aca ccc 7455	atc atg cag aag aaa	gtt gga cag atc atg	ctg atc ttg
Thr Pro 2440	Ile Met Gln Lys Lys	Val Gly Gln Ile Met	Leu Ile Leu 2450
gtg tct 7500	cta gct gca gta gta	gtg aac ccg tct gtg	aag aca gta
Val Ser 2455	Leu Ala Ala Val Val	Val Asn Pro Ser Val	Lys Thr Val 2465
cga gaa 7545	gcc gga att ttg atc	acg gcc gca gcg gtg	acg ctt tgg
Arg Glu 2470	Ala Gly Ile Leu Ile	Thr Ala Ala Ala Val	Thr Leu Trp 2480
gag aat 7590	gga gca agc tct gtt	tgg aac gca aca act	gcc atc gga
Glu Asn 2485	Gly Ala Ser Ser Val	Trp Asn Ala Thr Thr	Ala Ile Gly 2495
ctc tgc 7635	cac atc atg cgt ggg	ggt tgg ttg tca tgt	cta tcc ata
Leu Cys 2500	His Ile Met Arg Gly	Gly Trp Leu Ser Cys	Leu Ser Ile 2510
aca tgg 7680	aca ctc ata aag aac	atg gaa aaa cca gga	cta aaa aga
Thr Trp 2515	Thr Leu Ile Lys Asn	Met Glu Lys Pro Gly	Leu Lys Arg 2525
ggt ggg 7725	gca aaa gga cgc acc	ttg gga gag gtt tgg	aaa gaa aga
Gly Gly 2530	Ala Lys Gly Arg Thr	Leu Gly Glu Val Trp	Lys Glu Arg 2540
ctc aac 7770	cag atg aca aaa gaa	gag ttc act agg tac	cgc aaa gag
Leu Asn 2545	Gln Met Thr Lys Glu	Glu Phe Thr Arg Tyr	Arg Lys Glu 2555
gcc atc 7815	atc gaa gtc gat cgc	tca gcg gca aaa cac	gcc agg aaa
Ala Ile 2560	Ile Glu Val Asp Arg	Ser Ala Ala Lys His	Ala Arg Lys 2570
gaa ggc 7860	aat gtc act gga ggg	cat cca gtc tct agg	ggc aca gca
Glu Gly 2575	Asn Val Thr Gly Gly	His Pro Val Ser Arg	Gly Thr Ala 2585

REPLACEMENT SHEET

Figure 12 continued

aaa ctg	aga tgg ctg gtc gaa	cgg agg ttt ctc gaa	ccg gtc gga
7905			
Lys Leu	Arg Trp Leu Val Glu	Arg Arg Phe Leu Glu	Pro Val Gly
2590	2595	2600	
aaa gtg	att gac ctt gga tgt	gga aga ggc ggt tgg	tgt tac tat
7950			
Lys Val	Ile Asp Leu Gly Cys	Gly Arg Gly Gly Trp	Cys Tyr Tyr
2605	2610	2615	
atg gca	acc caa aaa aga gtc	caa gaa gtc aga ggg	tac aca aag
7995			
Met Ala	Thr Gln Lys Arg Val	Gln Glu Val Arg Gly	Tyr Thr Lys
2620	2625	2630	
ggc ggt	ccc gga cat gaa gag	ccc caa cta gtg caa	agt tat gga
8040			
Gly Gly	Pro Gly His Glu Glu	Pro Gln Leu Val Gln	Ser Tyr Gly
2635	2640	2645	
tgg aac	att gtc acc atg aag	agt gga gtg gat gtg	ttc tac aga
8085			
Trp Asn	Ile Val Thr Met Lys	Ser Gly Val Asp Val	Phe Tyr Arg
2650	2655	2660	
cct tct	gag tgt tgt gac acc	ctc ctt tgt gac atc	gga gag tcc
8130			
Pro Ser	Glu Cys Cys Asp Thr	Leu Leu Cys Asp Ile	Gly Glu Ser
2665	2670	2675	
tcg tca	agt gct gag gtt gaa	gag cat agg acg att	ccg gtc ctt
8175			
Ser Ser	Ser Ala Glu Val Glu	Glu His Arg Thr Ile	Arg Val Leu
2680	2685	2690	
gaa atg	gtt gag gac tgg ctg	cac cga ggg cca agg	gaa ttt tgc
8220			
Glu Met	Val Glu Asp Trp Leu	His Arg Gly Pro Arg	Glu Phe Cys
2695	2700	2705	
gtg aag	gtg ctc tgc ccc tac	atg ccg aaa gtc ata	gag aag atg
8265			
Val Lys	Val Leu Cys Pro Tyr	Met Pro Lys Val Ile	Glu Lys Met
2710	2715	2720	
gag ctg	ctc caa cgc cgg tat	ggg ggg gga ctg gtc	aga aac cca
8310			
Glu Leu	Leu Gln Arg Arg Tyr	Gly Gly Gly Leu Val	Arg Asn Pro
2725	2730	2735	

REPLACEMENT SHEET

Figure 12 continued

ctc tca cgg aat tcc acg cac gag atg tat tgg gtg agt cga gct
8355
Leu Ser Arg Asn Ser Thr His Glu Met Tyr Trp Val Ser Arg Ala
2740 2745 2750

tca ggc aat gtg gta cat tca gtg aat atg acc agc cag gtg ctc
8400
Ser Gly Asn Val Val His Ser Val Asn Met Thr Ser Gln Val Leu
2755 2760 2765

cta gga aga atg gaa aaa agg acc tgg aag gga ccc caa tac gag
8445
Leu Gly Arg Met Glu Lys Arg Thr Trp Lys Gly Pro Gln Tyr Glu
2770 2775 2780

gaa gat gta aac ttg gga agt gga acc agg gcg gtg gga aaa ccc
8490
Glu Asp Val Asn Leu Gly Ser Gly Thr Arg Ala Val Gly Lys Pro
2785 2790 2795

ctg ctc aac tca gac acc agt aaa atc aag aac agg att gaa cga
8535
Leu Leu Asn Ser Asp Thr Ser Lys Ile Lys Asn Arg Ile Glu Arg
2800 2805 2810

ctc agg cgt gag tac agt tcg acg tgg cac cac gat gag aac cac
8580
Leu Arg Arg Glu Tyr Ser Ser Thr Trp His His Asp Glu Asn His
2815 2820 2825

cca tat aga acc tgg aac tat cac ggc agt tat gat gtg aag ccc
8625
Pro Tyr Arg Thr Trp Asn Tyr His Gly Ser Tyr Asp Val Lys Pro
2830 2835 2840

aca ggc tcc gcc agt tcg ctg gtc aat gga gtg gtc agg ctc ctc
8670
Thr Gly Ser Ala Ser Ser Leu Val Asn Gly Val Val Arg Leu Leu
2845 2850 2855

tca aaa cca tgg gac acc atc acg aat gtt acc acc atg gcc atg
8715
Ser Lys Pro Trp Asp Thr Ile Thr Asn Val Thr Thr Met Ala Met
2860 2865 2870

act gac act act ccc ttc ggg cag cag cga gtg ttc aaa gag aag
8760
Thr Asp Thr Thr Pro Phe Gly Gln Gln Arg Val Phe Lys Glu Lys
2875 2880 2885

REPLACEMENT SHEET

Figure 12 continued

gtg gac 8805	acg aaa gct cct gaa	ccg cca gaa gga gtg	aag tac gtg
Val Asp 2890	Thr Lys Ala Pro 2895	Pro Pro Glu Gly Val 2900	Lys Tyr Val
ctc aat 8850	gag acc acc aac tgg	ttg tgg gcg ttt ttg	gcc aga gaa
Leu Asn 2905	Glu Thr Thr Asn Trp 2910	Leu Trp Ala Phe Leu 2915	Ala Arg Glu
aaa cgt 8895	ccc aga atg tgc tct	cga gag gaa ttc ata	aga aag gtc
Lys Arg 2920	Pro Arg Met Cys Ser 2925	Arg Glu Glu Phe Ile 2930	Arg Lys Val
aac agc 8940	aat gca gct ttg ggt	gcc atg ttt gaa gag	cag aat caa
Asn Ser 2935	Asn Ala Ala Leu Gly 2940	Ala Met Phe Glu Glu 2945	Gln Asn Gln
tgg agg 8985	agc gcc aga gaa gca	gtt gaa gat cca aaa	ttt tgg gag
Trp Arg 2950	Ser Ala Arg Glu Ala 2955	Val Glu Asp Pro Lys 2960	Phe Trp Glu
atg gtg 9030	gat gag gag cgc gag	gca cat ctg cgg ggg	gaa tgt cac
Met Val 2965	Asp Glu Glu Arg Glu 2970	Ala His Leu Arg Gly 2975	Glu Cys His
act tgc 9075	att tac aac atg atg	gga aag aga gag aaa	aaa ccc gga
Thr Cys 2980	Ile Tyr Asn Met Met 2985	Gly Lys Arg Glu Lys 2990	Lys Pro Gly
gag ttc 9120	gga aag gcc aag gga	agc aga gcc att tgg	ttc atg tgg
Glu Phe 2995	Gly Lys Ala Lys Gly 3000	Ser Arg Ala Ile Trp 3005	Phe Met Trp
ctc gga 9165	gct cgc ttt ctg gag	ttc gag gct ctg ggt	ttt ctc aat
Leu Gly 3010	Ala Arg Phe Leu Glu 3015	Phe Glu Ala Leu Gly 3020	Phe Leu Asn
gaa gac 9210	cac tgg ctt gga aga	aag aac tca gga gga	ggg gtc gag
Glu Asp 3025	His Trp Leu Gly Arg 3030	Lys Asn Ser Gly Gly 3035	Gly Val Glu

REPLACEMENT SHEET

Figure 12 continued

ggc ttg	ggc ctc	caa aaa	ctg	ggt tac	atc ctg	cgt	gaa gtt	ggc
9255								
Gly Leu	Gly Leu	Gln Lys	Leu	Gly Tyr	Ile Leu	Arg	Glu Val	Gly
3040			3045			3050		
acc cgg	cct ggg	ggc aag	atc	tat gct	gat gac	aca	gct ggc	tgg
9300								
Thr Arg	Pro Gly	Gly Lys	Ile	Tyr Ala	Asp Asp	Thr	Ala Gly	Trp
3055			3060			3065		
gac acc	cgc atc	acg aga	gct	gac ttg	gaa aat	gaa	gct aag	gtg
9345								
Asp Thr	Arg Ile	Thr Arg	Ala	Asp Leu	Glu Asn	Glu	Ala Lys	Val
3070			3075			3080		
ctt gag	ctg ctt	gat ggg	gaa	cat cgg	cgt ctt	gcc	agg gcc	atc
9390								
Leu Glu	Leu Leu	Asp Gly	Glu	His Arg	Arg Leu	Ala	Arg Ala	Ile
3085			3090			3095		
att gag	ctc acc	tat cgt	cac	aaa gtt	gtg aaa	gtg	atg cgc	ccg
9435								
Ile Glu	Leu Thr	Tyr Arg	His	Lys Val	Val Lys	Val	Met Arg	Pro
3100			3105			3110		
gct gct	gat gga	aga acc	gtc	atg gat	gtt atc	tcc	aga gaa	gat
9480								
Ala Ala	Asp Gly	Arg Thr	Val	Met Asp	Val Ile	Ser	Arg Glu	Asp
3115			3120			3125		
cag agg	ggg agt	gga caa	gtt	gtc acc	tac gcc	cta	aac act	ttc
9525								
Gln Arg	Gly Ser	Gly Gln	Val	Val Thr	Tyr Ala	Leu	Asn Thr	Phe
3130			3135			3140		
acc aac	ctg gcc	gtc cag	ctg	gtg agg	atg atg	gaa	ggg gaa	gga
9570								
Thr Asn	Leu Ala	Val Gln	Leu	Val Arg	Met Met	Glu	Gly Glu	Gly
3145			3150			3155		
gtg att	ggc cca	gat gat	gtg	gag aaa	ctc aca	aaa	ggg aaa	gga
9615								
Val Ile	Gly Pro	Asp Asp	Val	Glu Lys	Leu Thr	Lys	Gly Lys	Gly
3160			3165			3170		
ccc aaa	gtc agg	acc tgg	ctg	ttt gag	aat ggg	gaa	gaa aga	ctc
9660								
Pro Lys	Val Arg	Thr Trp	Leu	Phe Glu	Asn Gly	Glu	Glu Arg	Leu
3175			3180			3185		

REPLACEMENT SHEET

Figure 12 continued

agc cgc 9705	atg gct gtc agt gga	gat gac tgt gtg gta	aag ccc ctg
Ser Arg 3190	Met Ala Val Ser Gly 3195	Asp Asp Cys Val Val	Lys Pro Leu 3200
gac gat 9750	cgc ttt gcc acc tgg	ctc cac ttc ctc aat	gct atg tca
Asp Asp 3205	Arg Phe Ala Thr Ser 3210	Leu His Phe Leu Asn	Ala Met Ser 3215
aag gtt 9795	cgc aaa gac atc caa	gag tgg aaa cgc tca	act gga tgg
Lys Val 3220	Arg Lys Asp Ile Gln 3225	Glu Trp Lys Pro Ser	Thr Gly Trp 3230
tat gat 9840	tgg cag cag gtt cca	ttt tgc tca aac cat	ttc act gaa
Tyr Asp 3235	Trp Gln Gln Val Pro 3240	Phe Cys Ser Asn His	Phe Thr Glu 3245
ttg atc 9885	atg aaa gat gga aga	aca ctg gtg gtt cca	tgc cga gga
Leu Ile 3250	Met Lys Asp Gly Arg 3255	Thr Leu Val Val Pro	Cys Arg Gly 3260
cag gat 9930	gaa ttg gta ggc aga	gct cgc ata tct cca	ggg gcc gga
Gln Asp 3265	Glu Leu Val Gly Arg 3270	Ala Arg Ile Ser Pro	Gly Ala Gly 3275
tgg aac 9975	gtc cgc gac act gct	tgt ctg gct aag tct	tat gcc cag
Trp Asn 3280	Val Arg Asp Thr Ala 3285	Cys Leu Ala Lys Ser	Tyr Ala Gln 3290
atg tgg 10020	ctg ctt ctg tac ttc	cac aga aga gac ctg	cgg ctc atg
Met Trp 3295	Leu Leu Leu Tyr Phe 3300	His Arg Arg Asp Leu	Arg Leu Met 3305
gcc aac 10065	gcc att tgc tcc gct	gtc cct gtg aat tgg	gtc cct acc
Ala Asn 3310	Ala Ile Cys Ser Ala 3315	Val Pro Val Asn Trp	Val Pro Thr 3320
gga aga 10110	acc acg tgg tcc atc	cat gca gga gga gag	tgg atg aca
Gly Arg 3325	Thr Thr Trp Ser Ile 3330	His Ala Gly Gly Glu	Trp Met Thr 3335

REPLACEMENT SHEET

Figure 12 continued

aca gag gac atg ttg gag gtc tgg aac cgt gtt tgg ata gag gag
10155
Thr Glu Asp Met Leu Glu Val Trp Asn Arg Val Trp Ile Glu Glu
3340 3345 3350

aat gaa tgg atg gaa gac aaa acc cca gtg gag aaa tgg agt gac
10200
Asn Glu Trp Met Glu Asp Lys Thr Pro Val Glu Lys Trp Ser Asp
3355 3360 3365

gtc cca tat tca gga aaa cga gag gac atc tgg tgt ggc agc ctg
10245
Val Pro Tyr Ser Gly Lys Arg Glu Asp Ile Trp Cys Gly Ser Leu
3370 3375 3380

att ggc aca aga gcc cga gcc acg tgg gca gaa aac atc cag gtg
10290
Ile Gly Thr Arg Ala Arg Ala Thr Trp Ala Glu Asn Ile Gln Val
3385 3390 3395

gct atc aac caa gtc aga gca atc atc gga gat gag aag tat gtg
10335
Ala Ile Asn Gln Val Arg Ala Ile Ile Gly Asp Glu Lys Tyr Val
3400 3405 3410

gat tac atg agt tca cta aag aga tat gaa gac aca act ttg gtt
10380
Asp Tyr Met Ser Ser Leu Lys Arg Tyr Glu Asp Thr Thr Leu Val
3415 3420 3425

gag gac aca gta ctg tag atatttaatc aattgtaaat agacaatata
10428
Glu Asp Thr Val Leu
3430

agtatgcata aaagtgtagt tttatagtag tatttagtggt tgtagtgta aatagttaag
10488

aaaattttga ggagaaagtc aggcgggaa gttcccgcca ccggaagttg agtagacggt
10548

gtgcctgcg actcaacccc aggaggactg ggtgaacaaa gccgcgaagt gatccatgta
10608

agccctcaga accgtctcgg aaggaggacc ccacatgttg taacttcaaa gcccaatgtc
10668

agaccacgct acggcgtgct actctgcgga gaggcagtc tgcgatagtg cccagagag
10728

REPLACEMENT SHEET

Figure 12 continued

actgggttaa caaaggcaaa ccaacgcccc acgcggccct agccccggtg atggtgttaa
10788

ccagggcgaa aggactagag gttagaggag accccgcggt ttaaagtga cgccccagcc
10848

tgactgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa
10908

caccacaaca aaacagcata ttgacacctg ggatagacta ggagatcttc tgctctgcac
10968

aaccagccac acggcacagt gcgcgcgaaa tggaggctgg tggcgcgaga acacaggatc
11028

t
11029

REPLACEMENT SHEET

Figure 13 5kb C5 locus and PCR primers to amplify C5 arms (SEQ ID NO: 77)

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CTGAAATTGTAAATTTCTACATGTAGAGAAAGGTTTTGATATTGATGGTTTTTAAACAGAAACG
GACTTTAAACATTAAAGATGTACATCTCTTCCAAAACATATACTACCAAATTTGTCTTTGC
      10              20              30              40              50              60

TAGAAATTATATCAAGGGATAACATTTTATATGATATAGTTTTAAAGTGTAAGATGGAAT
ATCTTTAATATAGTTCCTTATTTGTAATAATACTATATCAAAATTTACATTTCTACCTTA
      70              80              90              100             110             120

TAAATTTTCATGTGCACAAGAGGCATAGGAGATAAAAGCATTTTCAGACTTTGTATAATGA
ATTTAAAGTACACGTGTTCTCGTATCCTCTATTTTCGTAAAAGTCTGAAACATATTACT
      130             140             150             160             170             180

AGGAATATGATCAAATAAACAGAAATCTGTTAGTTAGTTACTTGGATAAAATTAATCGAGA
TCCTTATACTAGTTTTATTTGTTCTTAGACAATCAATCAATGAACCTATTTAATTAGCTCT
      190             200             210             220             230             240

CGCGTGATAAAATGACTATGTACCGTTATTGCATGAACGATATTATAAATATAGTTCTC
GCGCACTATTTTACTGATACATGGCAATAACGTACTTGCTATAATTTTATATCCAAGAG
      250             260             270             280             290             300

(C5A1)  GGCCGAATTC
GTAGGAGAGAACTATTGACTATGGCAATGAATGTTAAATGTTTATCTTTGGATGAAGCTA
CATCCTCTCTTGATAACTGATACCGTTACTTACAATTTACAATATGAAACCTACTTCGAT
      310             320             330             340             350             360

TAAATATGCATTGGAATAATAATCCATTTAAAGAAAGGATTCAAATACTACAAAACCTAA
ATTTATACGTAAACCTTTTATTAGGTAATAATTCCTTCCTAAGTTTATGATGTTTTGGATT
      370             380             390             400             410             420

GCGATAATATGTTAACTAAGCTTATTCCTTAACGACGCTTTAAATATACACAAAATAACAT
CGCTATTTATACAATTGATTGGAATAAGAATTCTTCGCAAAATTTATATGTGTTTATTGTGTA
      430             440             450             460             470             480

AATTTTTGTATAACCTAACAAATAACTAAAACATAAAAAATAAAAAAGGAAATGTAATAT
TTAAAAACATATTGGATTGTTTATTGATTTTGTATTTTATTTTCTTTACATTATA
      490             500             510             520             530             540

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REPLACEMENT SHEET

Figure 13 continued

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CGTAATTTATTTTACTCAGGAATGGGGTTAAATATTTATATCACGTGTATATCTATACTGT
GCATTAAATAAAATGAGTCCTTACCCCAATTTATAAATATAGTGCACATATAGATATGACA
550          560          570          580          590          600

TATCGTATACTCTTTTACAAATTAATACGAATATGCAAGAGATAATAAGATTACGTATT
ATAGCATATGAGAAATGTTAATGATAATGCTTATACGTTCTCTATTATTCTAATGCATAA
610          620          630          640          650          660

TAAGAGAATCTTGTCTATGATAATTGGGTACGACATAGTGATAAATGCTATTTTCGCATCGT
ATTCTCTTAGAAGACAGTACTATTAACCCATGCTGTATCACTATTTACGATAAAGCGTAGCA
670          680          690          700          710          720

TACATAAAGTCAGTTGGAAAGATGGATTTGACAGATGTAACCTTAATAGGTGCAAAAATGT
ATGTATTTTCAGTCAACCTTTCTACCTAAACTGTCTACATTGAATTTATCCACGTTTTTACA
730          740          750          760          770          780

TAAATAACAGCATTTCTATCGGAAGATAGGATACAGTTATATTATACAAAAATCACTGGT
ATTTATTTGTGCTAAGATAGCCTTCTATCCTATGGTCAATATAAATATGTTTTTAGTGACCA
790          800          810          820          830          840

TGGATAAACAGATTCTGCAATATTCGTAAGAGATGAAGATTACTGCGAATTTGTAAACT
ACCTATTTTGTCTAAGACGTTATAAGCATTCTTCTACTTCTAATGACGCTTAAACATTTGA
850          860          870          880          890          900

ATGACAATAAAAGCCATTTTATCTCAACGACATCGTGTAATTTCTTCCATGTTTTATGTAT
TACTGTTATTTTTTCGTTAAATAGAGTTGCTGTAGCACATTAAGAAGGTACAAAAACATA
910          920          930          940          950          960

GTGTTTCAGATATTATGAGATTACTATAAACTTTTTGTATACCTTATATTCGTAACCTAT
CACAAAGTCTATAATACTCTAATGATATTTGAAAAACATATGAATATAAGGCATTTGATA
970          980          990          1000          1010          1020

ATTAATCATGAAGAAAATGAAAAAGTATAGAAGCTGTTACAGAGCGGTTGTTGAAAACAA
TAATTAGTACTCTTTTACTTTTTTCATATCTTCGACAAGTGCTCGCCCAACAACCTTTGTT
1030          1040          1050          1060          1070          1080

CAAAATTTATACATTCAAGATGGCTTACATATACGTCGTGAGGCTATCATGGATAATGAC

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REPLACEMENT SHEET

Figure 13 continued

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G T T T T A A T A T S T A A G T T C T A C C G A A T S T A T A T G C A G A C A C T C C G A T A G T A C C T A T T A C T G
      1090           1100           1110           1120           1130           1140
A A T G C A T C T C T A A A T A G G T T T T T G G A C A A T G S A T T C G A C C C T A A C A C G G A A T A T G G T A C T
T T A C G T A G A G A T T T A T C C A A A A A C C T G T T A C C T A A G C T G G G A T T G T G C C T T A T A C C A T G A
      1150           1160           1170           1180           1190           1200

C T A C A A T C T C C T C T T G A A A T G G C T G T A A T G T T C A A G A A T A C C G A G G C T A T A A A A A T C T T G
G A T G T T A G A G A G A A C T T T A C C G A C A T T A C A A G T T C T T A T G G C T C C G A T A T T T T T A G A A C
      1210           1220           1230           1240           1250           1260

A T G A G G T A T G G A G C T A A A C C T G T A G T T A C T G A A T G C A C A A C T T C T T G T C T G C A T G A T G C G
T A C T C C A T A C C T C G A T T T G G A C A T C A A T G A C T T A C G T G T T G A A G A A C A G A C G T A C T A C G C
      1270           1280           1290           1300           1310           1320

G T G T T G A G A G A C G A C T A C A A A A T A G T G A A A G A T C T G T T G A A G A A T A A C T A T G T A A A C A A T
C A C A A C T C T C T G C T G A T G T T T T A T C A C T T T C T A G A C A A C T T C T T A T T G A T A C A T T T G T T A
      1330           1340           1350           1360           1370           1380

G T T C T T T A C A G C G G A G G C T T T A C T C C T T T G T G T T T G G C A G C T T A C C T T A A C A A A G T T A A T
C A A G A A A T G T C G C C T C C G A A A T G A G G A A A C A C A A A C G T C G A A T G S A A T T G T T T C A A T T A
      1390           1400           1410           1420           1430           1440

T T G G T T A A A C T T C T A T T G G C T C A T T C G G C G G A T G T A G A T A T T T C A A A C A C G G A T C G G T T A
A A C C A A T T T G A A G A T A A C C G A G T A A G C C G C C T A C A T C T A T A A A G T T T G T G C C T A G C C A A T
      1450           1460           1470           1480           1490           1500

A C T C C E C T A C A T A T A G C C G T A T C A A A T A A A A A T T T A A C A A T G G T T A A A C T T C T A T T G A A C
T G A G G A G A T G T A T A T C G G C A T A G T T T A T T T T A A A T T G T T A C C A A T T T G A A G A T A A C T T G
      1510           1520           1530           1540           1550           1560

A A A G G T G C T G A T A C T G A C T T G C T G G A T A A C A T G G G A C G T A C T C C T T A A T G A T C G C T G T A
T T T C C A C G A C T A T G A C T G A A C G A C C T A T T G T A C C C T G C A T G A G G A A A T T A C T A G C G A C A T
      1570           1580           1590           1600           1610           1620

C A A T C T G G A A A T A T T G A A A T A T G T A G C A C A C T A C T T A A A A A A A T A A A A T G T C C A G A A C T
G T T A G A C C T T T A T A A C T T T A T A C A T C G T G T G A T G A A T T T T T T T A T T T T A C A G G T C T T G A
      1630           1640           1650           1660           1670           1680

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REPLACEMENT SHEET

Figure 13 continued

GGGAAAAATTGATCTTCCAGCTGTAATTCATGGTAGAAAAAGTGTCTCAGGCTACTTT
 CCGCTTTTTCAGTACGAACGGTCGACATTAGTACCATCTTTTCTCAGCAGTCCGATGAAA
 1690 1700 1710 1720 1730 1740

TCAACAAAGGAGCAGATGTAACTACATCTTTGAAAGAAATGGAAAATCATATACTGTTT
 AGTTGTTTCTCCTCGTCTACATTGATGTAGAACTTTCTTTTACCTTTTAGTATATGACAAA
 1750 1760 1770 1780 1790 1800

TGGAATTGATTAAGAAAGTTACTCTGAGACACAAAAGAGGTAGCTGAAGTGGTACTCTC
 ACCTTAACTAATTTCTTTCAATGAGACTCTGTGTTTTCTCCATCGACTTCACCATGAGAG
 1810 1820 1830 1840 1850 1860

C5 ORF
 MET GLN ASN ASP ASP CYS GLU ALA ARG SER ARG GLU ILE THR LEU TYR ASP PHE LEU
 AAAATGCAGAACCGATGACTGCGAAGCAAGAAGTAGAGAAATAACACTTTTATGACTTTCTTT
 TTTTACGTCTTGCTACTGACGCTTCGTTCTTTCATCTCTTTATTGTGAAATACTGAAAGAA
 1870 1880 1890 1900 1910 1920

C CATGCACTGATTAATCGA TATTTT CCATGCGGCC (C5B1)

SER CYS ARG LYS ASP ARG ASP ILE MET MET VAL ILE ASN ASN SER ASP ILE ALA SER LYS
 AGTTGTAGAAAAAGATAGAGATATAATGATGGTCATAAAATACTCTGATATTGCAAGTAAA
 TCAACATCTCTTCTATCTCTATTAATTAACAGTATTTATTGAGACTATAACGTTTCTTTT
 1930 1940 1950 1960 1970 1980

CYS ASN ASN LYS LEU ASP LEU PHE LYS ARG ILE VAL LYS ASN ARG LYS LYS GLU LEU ILE
 TGCAATAATAAGTTAGATTTTATTTAAAAGGATAGTTAAAAATAGAAAAAAGAGTTAATT
 ACGTTATTATTCAATCTAAATAAATTTTCTTATCAATTTTATCTTTTTTCTCAATTAA
 1990 2000 2010 2020 2030 2040

CYS ARG VAL LYS ILE ILE HIS LYS ILE LEU LYS PHE ILE ASN THR HIS ASN ASN LYS ASN
 TGTAGGGTTAAATAATACATAAGATCTTAAATTTATAAATACGCATAATAATAAAAAAT
 ACATCCCAATTTTATTATGTTCTTAGAATTTTAAATTTTATGCGTATTATTATTTTTA
 2050 2060 2070 2080 2090 2100

(C5C1) SGATCTCGGGTTTTTA GACTAGTTAATCAGGGCCG
 ARG LEU TYR LEU LEU PRO SER GLU ILE LYS PHE LYS ILE PHE THR TYR LEU THR TYR LYS
 AGATTATACCTTATTACCTTCAGAGATAAAATTTAAGATATTTACTTATTTAACTTTATAA
 TCTAATATGAATAATGGAAGTCTCTATTTTAAATTTCTATAAATGAATAAATGAATATTT
 2110 2120 2130 2140 2150 2160

ASP LEU LYS CYS ILE ILE SER LYS ***
 SATCTAAATGCAATATTTCTAAATAATGAAAAAAGTACATCATGAGCAACGCGTTAGT
 CTAGATTTTACGTATTAAGAGATTTTACTTTTCTCATGTAGTACTCGTTGCGCAATCA
 2170 2180 2190 2200 2210 2220

REPLACEMENT SHEET

Figure 13 continued

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ATATTTTACAATGGAGATTAAAGCTCTATACCGTTCCTATGTTTATTGATTCAGATGATGT
TATAAAATGTTACCTCTAATTGGCGAGATATGGCAAGATACAAAATAACTAGTCTACTACA
2230      2240      2250      2260      2270      2280
TTTAAAAAGAAAGTTATTGAATATGAAAACCTTTAATGAAGATGAAGATGACGACGATGA
AAATCTTTTCTTCAATAACTTATACTTTTGAAATTACTTCTACTTCTACTGCTGCTACT
2290      2300      2310      2320      2330      2340

TTATTGTTGTAAATCTGTTTTAGATGAAGAAGATGACGCGCTAAAGTATACTATGGTTAC
AATAACAACATTTAGACAAAATCTACTTCTTCTACTGCGCGATTTCATATGATACCAATG
2350      2360      2370      2380      2390      2400

AAAGTATAAGTCTATACTACTAATGGCGACTTGTGCAAGAAGGTATAGTATAGTGAAAAAT
TTTCATATTGAGATATGATGATTACCGCTGAACACGTTCTTCCATATCATATCACTTTTA
2410      2420      2430      2440      2450      2460

GTTGTTAGATTATGATTATGAAAAACCAAATAAATCAGATCCATATCTAAAGGTATCTCC
CAACAATCTAATACTAATACTTTTGGTTTTATTAGTCTAGGTATAGATTCCATAGAGG
2470      2480      2490      2500      2510      2520

TTTGCACATAATTTTCATCTATTCCCTAGTTTGAATACTTTTTCATTATATTTGTTTACAGC
AAACGTGTATTTAAAGTAGATAAGGATCAAACTCTTTATGAAAGTAATATAAACAAATGTCTG
2530      2540      2550      2560      2570      2580
GACGTCGG (C5D1)

TGAAGACGAAAAAATATATCGATAATAGAAGATTATGTTAACTCTGCTAATAAGATGAA
ACTTCTGCTTTTTTATATAGCTATTATCTTCTAATACAATTGAGACGATTATTCTACTT
2590      2600      2610      2620      2630      2640

ATTGAATGAGTCTGTGATAATAGCTATAATCAGAGAAGTTCTAAAAGGAAATAAAATCT
TAACCTACTCAGACACTATTATCGATATTAGTCTCTTCAAGATTTTCTTTTATTTTTAGA
2650      2660      2670      2680      2690      2700

AACTGATCAGGATATAAAAACATTTGGCTGATGAAATCAACAAGGAGGAACTGAATATAGC
TTGACTAGTCCATATTTTTGTAAACCGACTACTTTAGTTGTTCTCTCTTGACTTATATCG
2710      2720      2730      2740      2750      2760

TAAACTATTGTTAGATAGAGGGGCCAAAGTAAATTACAAGGATGTTTACGGTTCTTTCAGC
ATTTGATAACAATCTATCTCCCCGGTTTCATTTAATGTTTCTACAATGCCAAGAAGTCTG
2770      2780      2790      2800      2810      2820

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REPLACEMENT SHEET

Figure 13 continued

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TCTCCATAGAGCTGCTATTGGTAGGAAACAGGATATGATAAAGCTGTTAATCGATCATGG
AGAGGTTATCTCGACGATAACCATCCTTTGTCCTATACTATTTTCGACAATTTAGCTAGTACC
2830      2840      2850      2860      2870      2880
AGCTGATGTTAAACTCTTTAACTATTGCTAAAGATAATCTTATTTAAAAAATAATATCA
TCGACTACATTTGAGAAATTGATAACGATTTCATTAGAAATAATTTTTTTTATTATAGT
2890      2900      2910      2920      2930      2940

CGTTTAGTAATATTAAAAATATATTAATAACTCTATTACTAATAACTCCAGTGGATATGAA
GC AAA TCATTATAATTTTATATAATTATTGAGATAATGATTATTGAGGTCCACCTTACTT
2950      2960      2970      2980      2990      3000

CATAATACGAAGTTTATACATTCTCATCAAAATCTTATTGACATCAAGTTAGATTGTGAA
GTATTATGCTTCAAATATGTAAGAGTAGTTTTAGAAATAACTGTAGTTCAATCTAACACTT
3010      3020      3030      3040      3050      3060

AATGAGATTATGAAATTAAGGAATACAAAAATAGGATGTAAGAACCTTACTAGAATGTTTT
TTACTCTAATACTTTTAATTCCTTATGTTTTATCCTACATTCCTGAATGATCTTACAAAA
3070      3080      3090      3100      3110      3120

ATCAATAATGATATGAATACAGTATCTTAGGGCTATAAAACAATGAAACGATTAAAAATTAT
TAGTTATTACTATACTTATGTCATAGATCCCGATATTTGTTACTTTGCTAATTTTTTAATA
3130      3140      3150      3160      3170      3180

AAAAATCATTTCCCTATATATAATACGCTCATAGAAAAATTCATTTCTGAAAGTATACTA
TTTTTAGTAAAGGGATATATATTATGCGAGTATCTTTTTAAGTAAAGACTTTCATATGAT
3190      3200      3210      3220      3230      3240

AGACACGAATTTATTGGATGGAGTTATAAATCTTTTTCAAGGATTCAATAATAAATTGCCT
TCTGTGCTTAATAACCTACCTCAATATTTAAGAAAAGTTTCCTAAGTTATTATTTAACGGA
3250      3260      3270      3280      3290      3300

TACGAGATTTCAGTACATTATACTGGAGAATCTTAATAACCATGAACATAAAAAAATTTTA
ATGCTCTAAGTCATGTAATATGACCTCTTAGAATTATTGGTACTTGATTTTTTTTAAAAAT
3310      3320      3330      3340      3350      3360

GATAATATACATTTAAAAAGGTAATAGATCATCTGTTATTATAAGCAAAGATGCTTGTTG
CTATTATATGTAATTTTTCCATTTTATCTAGTAGACAATAATATTCGTTTCTACGAACAAC
3370      3380      3390      3400      3410      3420

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REPLACEMENT SHEET

Figure 13 continued

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CCAATAATATACAAACAGGTATTTGTTTTATTTTTAACTACATATTGATGTTTCATTCTC
GGTTATATATAGTTGTCCATAAACAAAAATAAAAAATTGATGTATAAACTACAAGTAAGAG
      3430              3440              3450              3460              3470              3480
TTTATATAGTATACACAGAAAAATTCATAATCCACTTAGAATTTCTAGTTATCTAGTTTTT
AAATATATCATATGTGTCTTTTAAAGTATTAGGTGAATCTTAAAGATCAATAGATCAAAAA
      3490              3500              3510              3520              3530              3540

CTAGAATATTGTACTTTATTTCTAATGGAATGGCTCTCCAGCCTAGTAATTTATTAATGT
GATCTTTATAACATGAAATAAAGATTACCTTACCAGAGAGGTCGGATCATTAAATAATTACA
      3550              3560              3570              3580              3590              3600

TAGCTGATATCTTGAAATCAGGATATTCTGCTCCGTGAAGAGAAAGTCCTCCAAAGTTGT
ATCGACATATAGAACTTTAGTCTCTATAAGACGAGGCACCTTCTCTTCAGGAGGTTTCAACA
      3610              3620              3630              3640              3650              3660

ATATTTCCATCACTTTTCATGGCTTCTCTCTTCCATAGTGTCTTCTATAAGCTGTCTATAT
TATAAAGGTAGTGAAAGTACCGAAGGAGAAAGGTATCACAGAAGATATTTCGACAGATATA
      3670              3680              3690              3700              3710              3720

ATTGTAAACTTTTCTGGTTTTATGCATTTTAAACATTTAGCAATCTCATTTTCATCACAA
TAACATTTGAAAAGACCAAAATACGTAAAAATTTGTAATCGTTAGAGTAAAAGTAGTGTT
      3730              3740              3750              3760              3770              3780

TTAAGGCACAAATCTAACATGGAATGTCTACCATAACCCAATAAGGTTTTTTCATTTCTT
AATTCGGTGTTTAGATTGTACCTTACAGATGGTATTGGGTTATTCCAAAAAAGTAAAGGA
      3790              3800              3810              3820              3830              3840

CTATCTCTAATACACACTGTTCTTTCCAGACTTTCAACACGCTGCTATTTTCTATTTTAT
GATAGAGATTATGTGTGACAAGAAAGGTCGAAAAGTTGTGCGACGATAAAAGATAAAATA
      3850              3860              3870              3880              3890              3900

TCAAGTCCATATTATAAGCGTCCTTGTAGACACTTCATAATGTTTGCAATTCGGAATCA
AGTTCAGGTATAATATTTCGCAGGAACAATCTGTGAAGTATTACAAACGTAAGACCTTAGT
      3910              3920              3930              3940              3950              3960

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REPLACEMENT SHEET

Figure 13 continued

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TCATGTTAGATACTATTAATTTAGCTACTTCTATGTTGTCATCAAAAGAGTTGCTATCTG
AGTACAATCTATGATAATTAATTCGATGAAGATACAAACAGTAGTTTTCTCAACGATAGAC
          3970          3980          3990          4000          4010          4020

TAATTACACTAAGAGGTGTATCACCTGATAAAGAAGTAATAGAGACATCTGCTCTGAATT
ATTAATGTGATTCTCCACATAGTGGACTATTTCTTCATTATCTCTGTAGACGAGACTTAA
          4030          4040          4050          4060          4070          4080

TAAGCAATACCTCAATAACTTCTTTTGAAGATGACTTTGCAGCTAAAAATAATGGAGTTC
ATTCGTTATGGAGTTTATGAAGAAAACTTCTACTGAAACGTCGATTTTTTATTACCTCAAG
          4090          4100          4110          4120          4130          4140

TCTCTAAAACATCCCTTGAGTTTATATTAGCCCCGFAACTAATGAGTAGTTCTGTTATAT
AGAGATTTTGTAGGGAACCTCAAAATATAATCGGGGCATTGATTACTCATCAAGACAATATA
          4150          4160          4170          4180          4190          4200

CTTTGGAATCTATTGATATATTATTAATTACAATTGTCATGCTGACATATATAGACATCA
GAAACCTTAGATAACTATATAATAAATTAATGTTAACAGTACGACTGTATATATCTGTAGT
          4210          4220          4230          4240          4250          4260

TAATATGATGAAAAATATGAAAAATATAAGTGCACGTTTACTGTTACTATGATTGTGATAT
ATTATACTACTTTTTTATCTTTTATATTTCACGTGCAAAATGACAATGATACTAACACTATA
          4270          4280          4290          4300          4310          4320

CGATATGAGTTCTTTTAATAAAAGTACTGAAATAGATATAATGCAGATATGATTGATATTT
GCTATACTCAAGAAAAATTTTTTCATGACTTTATCTATATTACGTCTATACTAACTATAAA
          4330          4340          4350          4360          4370          4380

TAAAAAGTTGAAAAAAAATATGCCCTGTTTACAAATACTATTTGGAAATATTTCTGTAATA
ATTTTTCAACTTTTTTTTATACGGGGACAAATGTTTTATGATAAACCTTTATAAGACATTAT
          4390          4400          4410          4420          4430          4440

AAGTAATAGTGATATGTCAGTCACGATGGATTGCCAAATTGATCATATGAGTATAGATAA
TTCATTATCACTATACAGTCAGTGCTACCTAAACGGTTAACTAGTATACTCATATCTATT
          4450          4460          4470          4480          4490          4500

CATAAACGAGTATAATAAAAAATGGATATACTAGACTCTATATAGAGGTAGCCATGAAAAA
GTTTTGCTCATATTTATTTTACCTATATGATCTGAGATATATCTCCATCGGTACTTTTT
          4510          4520          4530          4540          4550          4560

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REPLACEMENT SHEET

Figure 13 continued

ACGTAAAAACGTAGATAGACTTTTATATCTCGGAGCTGATCCGAATCTGGCTAGTGTAGA
TGCATTTTTCATCTATCTGAAAATATAGAGCCTCGACTAGGCTTAGACCGATCACATCT
4570 4580 4590 4600 4610 4620

TTCTGATTGTCTCTTCATATTGCTGTTAGGAATGGTAGTTTTAAGATAATAAGATCATT
AAGCATAACAGGAGAAGTATAACGACAATCCTTACCATCAAATTTCTATTATTCTAGTAA
4630 4640 4650 4660 4670 4680

GTGAAATATSGTGCTAATATAAATCAAGAATGTCATGAAGGAGATACTGCTTTGATGAT
CAACTTTATACCACGATTATATTTAGTTCTTACAGTACTTCTCTATGACGAACTACTA
4690 4700 4710 4720 4730 4740

GGCTATATCATTAGGTAATTATACAGCATGTAAACACTTCTAGATAACAACGCCGATCC
CCGATATAGTAATCCATTAATATGTCGTACATTTTGTGAAGATCTATTGTTGCGGCTAGG
4750 4760 4770 4780 4790 4800

TAATTATGTTAACTATTACGGTATAGTTCCGCTTATTAGAGCAATTATATGTGAAAAGCC
ATTAATACAATTGATAATGCCATATCAAGGCGAATAATCTCGTTAATATACACTTTTCGG
4810 4820 4830 4840 4850 4860

TGACATAGTTAGACTGCTATTAGATAGAGGAGCTAATTGCAACCACTTAATTACAAAAA
ACTGTATCAATCTGACGATAATCTATCTCCTCGATTAAACGTTGGTGAATTAATGTTTTT
4870 4880 4890 4900 4910 4920

CGGTAGAACCCTATACTGCTTTAGAGAGTCTTAGGAATTGCTTTTTTAAAGACAATTCTTC
GCCATCTTGGATATGACGAAATCTCTCAGAATCCTTAACGAAAAAATTTCTGTTAAGAAG
4930 4940 4950 4960 4970 4980

ATCATTGTCGATACTAATAT
TAGTAACAGCTATGATTATA
4990 5000